

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2005, 15:23:29 ; Search time 164 Seconds  
(without alignments)  
221.680 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVRDLVVAAATPTSLRI.....VTKSDTYKYDDPISINYRT 94

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*

2: geneseqp1990s:\*

3: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

6: geneseqp2003as:\*

7: geneseqp2003bs:\*

8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	494	100.0	94	5	Abb78898 Tumour ne
2	494	100.0	94	5	Abb78921 Tumour ne
3	489	99.0	94	5	Abb78939 Tumour ne
4	489	99.0	94	5	Abb78919 Tumour ne
5	489	99.0	94	5	Abb78920 Tumour ne
6	488	98.8	94	5	Abb78911 Tumour ne
7	486	98.4	94	5	Abb78915 Tumour ne
8	484	98.0	94	5	Abb78940 Tumour ne
9	484	98.0	94	5	Abb78912 Tumour ne
10	483	97.8	94	5	Abb78916 Tumour ne
11	483	97.8	94	5	Abb78918 Tumour ne
12	481	97.4	94	5	Abb78899 Tumour ne
13	478	96.8	94	5	Abb78917 Tumour ne
14	463	93.7	94	5	Abb78922 Tumour ne
15	446	90.3	94	5	Abb78923 Tumour ne
16	443	89.7	94	5	Abb78949 Tumour ne
17	439	88.9	94	5	Abb78873 Tumour ne
18	437.5	88.6	93	5	Abb78869 Tumour ne
19	437	88.5	93	5	Abb78868 Tumour ne
20	431	87.2	94	5	Abb78872 Tumour ne
21	419	84.8	94	5	Abb78942 Tumour ne
22	417	84.4	94	5	Abb78870 Tumour ne
23	416	84.2	94	5	Abb78900 Tumour ne
24	415	84.0	94	5	Abb78871 Tumour ne
25	406	82.2	94	5	Abb78895 Tumour ne

ALIGNMENTS

RESULT 1

Abb78898  
ID Abb78898 standard; peptide; 94 AA.  
AC Abb78898;  
XX  
DT 30-JUL-2002 (first entry)  
DE Tumour necrosis factor-alpha binding amino acid sequence T10.06.  
XX  
KW Protein scaffold; antibody; binding protein; immunoglobulin; tumour necrosis factor alpha; TNF-alpha; protein framework.  
XX Homo sapiens.  
OS Synthetic.  
XX  
FN WO200232925-A2.  
XX  
PD 25-APR-2002.  
XX  
PF 16-OCT-2001; 2001WO-US032233.  
XX  
PR 16-OCT-2000; 2000US-00688566.  
XX (PHYL-) PHYLLOS INC.  
PI Lipovsek D, Wagner RW, Kuimelis RG;  
XX  
DR WPI; 2002-444238/47.  
XX  
PT New non-antibody proteins having an immunoglobulin fold, useful in research, therapeutic or diagnostic fields, particularly as scaffolds for designing proteins with specific properties, e.g. for binding any antigen of interest.  
XX  
PS Claim 47; Fig 25; 94pp; English.  
XX  
CC The present invention describes a non-antibody protein, comprising a domain having an immunoglobulin-like fold, derived from a reference protein having a mutated amino acid sequence, where the non-antibody protein binds with a Kd at least as tight as 10 nM to a compound that is not bound as tightly by the reference protein. The non-antibody protein is useful as scaffolds for selecting or designing a protein framework with specific and favourable properties, e.g. for binding any antigen of interest, or for destroying or inactivating antibody molecules. The non-antibody protein is also useful in all areas where antibodies are used, e.g. research, therapeutic or diagnostic fields, and for screening novel binding proteins useful in the above-mentioned fields. The present

26 402 81.4 94 5 ABB78941  
27 397 80.4 94 5 ABB78901  
28 395 80.0 76 5 ABB78897  
29 393 79.6 94 5 ABB78880  
30 392 79.4 94 5 ABB78879  
31 392 79.4 94 5 ABB78928  
32 390 78.9 94 5 ABB78954  
33 390 78.9 94 5 ABB78910  
34 389 78.7 94 5 ABB78881  
35 389 78.7 94 5 ABB78909  
36 388 78.5 94 5 ABB78950  
37 388 78.5 94 5 ABB78876  
38 387.5 78.4 93 5 ABB78896  
39 385 77.9 94 5 ABB78864  
40 384 77.7 94 5 ABB78867  
41 384 77.7 94 5 ABB78904  
42 382.5 77.4 93 5 ABB78878  
43 382 77.3 94 5 ABB78877  
44 380 76.9 94 5 ABB78866  
45 374 75.7 94 5 ABB78929

Abb78941 Tumour ne  
Abb78901 Tumour ne  
Abb78897 Tumour ne  
Abb78880 Tumour ne  
Abb78879 Tumour ne  
Abb78928 Tumour ne  
Abb78954 Tumour ne  
Abb78910 Tumour ne  
Abb78881 Tumour ne  
Abb78909 Tumour ne  
Abb78950 Tumour ne  
Abb78876 Tumour ne  
Abb78896 Tumour ne  
Abb78864 Tumour ne  
Abb78867 Tumour ne  
Abb78904 Tumour ne  
Abb78878 Tumour ne  
Abb78877 Tumour ne  
Abb78866 Tumour ne  
Abb78929 Tumour ne

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 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX Sequence 94 AA;  
 SQ

Query Match 100.0%; Score 494; DB 5; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e-49; Indels 0; Gaps 0;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQOEFTVPWPWASITATIS 60  
 DB 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQOEFTVPWPWASITATIS 60  
 QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 DB 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 2  
 ABB78921  
 ID ABB78921 standard; peptide; 94 AA.  
 XX  
 AC ABB78921;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Tumour necrosis factor-alpha binding amino acid sequence T14.26.  
 XX  
 KW Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200232925-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032233.  
 XX  
 PR 16-OCT-2000; 2000US-00688566.  
 XX  
 PA (PHYL-) PHYLLOS INC.  
 XX  
 PI Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
 DR

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 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.

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 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX Sequence 94 AA;  
 SQ

Query Match 100.0%; Score 494; DB 5; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e-49; Indels 0; Gaps 0;  
 Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQOEFTVPWPWASITATIS 60  
 DB 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQOEFTVPWPWASITATIS 60  
 QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 DB 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 3  
 ABB78939  
 ID ABB78939 standard; peptide; 94 AA.  
 XX  
 AC ABB78939;  
 XX  
 DT 30-JUL-2002 (first entry)  
 XX  
 DE Tumour necrosis factor-alpha binding amino acid sequence M12.01.  
 XX  
 KW Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 XX  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200232925-A2.  
 XX  
 PD 25-APR-2002.  
 XX  
 PF 16-OCT-2001; 2001WO-US032233.  
 XX  
 PR 16-OCT-2000; 2000US-00688566.  
 XX  
 PA (PHYL-) PHYLLOS INC.  
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 PI Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
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 CC protein having a mutated amino acid sequence, where the non-antibody  
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 CC with specific and favourable properties, e.g. for binding any antigen of  
 CC interest, or for destroying or inactivating antibody molecules. The non-

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 CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
 CC binding proteins useful in the above-mentioned fields. The present  
 CC proteins have thermodynamic properties superior to those of natural  
 CC antibodies, and can be evolved rapidly in vitro. The present natural  
 CC antibody mimics exhibit improved biophysical properties, such as  
 CC stability under reducing conditions and solubility at high  
 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. *Escherichia coli*), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;  
 Best Local Similarity 97.9%; Pred. No. 3.9e-49;  
 Matches 92; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 4

ABB78919  
 ID ABB78919 standard; peptide; 94 AA.

XX ABB78919;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.14.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.  
 OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

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 PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
 PT designing proteins with specific properties, e.g. for binding any antigen  
 PT of interest.

PS Claim 47; Fig 25; 94pp; English.

XX The present invention describes a non-antibody protein, comprising a  
 CC domain having an immunoglobulin-like fold, derived from a reference

CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
 CC is useful as scaffolds for selecting or designing a protein framework  
 CC with specific and favourable properties, e.g. for binding any antigen of  
 CC interest, or for destroying or inactivating antibody molecules. The non-  
 CC antibody protein is also useful in all areas where antibodies are used,  
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 CC proteins have thermodynamic properties superior to those of natural  
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 CC antibody mimics exhibit improved biophysical properties, such as  
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 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
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 CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-49;  
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRITYGTGNSPVQETVPPWASIIATIS 60  
 Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRITYGTGNSPVQETVPPWASIIATIS 60  
 .Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
 Db 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94

RESULT 5

ABB78920  
 ID ABB78920 standard; peptide; 94 AA.

XX ABB78920;

XX 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence T14.23.

XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.  
 OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

XX (PHYL-) PHYLLOS INC.

XX Lipovsek D, Wagner RW, Kuimelis RG;

XX WPI; 2002-444238/47.

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 CC protein having a mutated amino acid sequence, where the non-antibody  
 CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
 CC not bound as tightly by the reference protein. The non-antibody protein  
 CC is useful as scaffolds for selecting or designing a protein framework  
 CC with specific and favourable properties, e.g. for binding any antigen of  
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 CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
 CC binding proteins useful in the above-mentioned fields. The present  
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 CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
 CC antibody mimics exhibit improved biophysical properties, such as  
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 CC concentrations. In addition, these molecules are readily expressed and  
 CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
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 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX Sequence 94 AA;

Query Match 99.0%; Score 489; DB 5; Length 94;  
 Best Local Similarity 98.9%; Pred. No. 3.9e-49;  
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 |||||  
 DB 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 |||||

QY 61 GLKPGVDYTTITVAVTDSKYDDPISINVRT 94  
 |||||  
 DB 61 GLKPGVDYTTITVAVADKSDTYKYDDPISINVRT 94  
 |||||

RESULT 6  
 ABB78911  
 ID ABB78911 standard; peptide; 94 AA.  
 AC ABB78911;  
 DT 30-JUL-2002 (first entry)  
 XX Tumour necrosis factor-alpha binding amino acid sequence S08.02.  
 XX Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200232925-A2.  
 XX 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032233.  
 XX 16-OCT-2000; 2000US-00688566.  
 XX (PHYL-) PHYLLOS INC.  
 XX Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
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 CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
 CC reticulocyte lysate system). Furthermore, these proteins are extremely  
 CC amenable to affinity maturation techniques involving multiple cycles of  
 CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
 CC phage display or yeast display systems. The present sequence is used in  
 CC the exemplification of the present invention  
 XX Sequence 94 AA;

Query Match 98.8%; Score 488; DB 5; Length 94;  
 Best Local Similarity 98.9%; Pred. No. 5.1e-49;  
 Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
 |||||  
 DB 1 VSDVPRDLEVVAATPTSLISWNRSLQSRYYRITYGETGNSPVQELTVPWASITATIS 60  
 |||||

QY 61 GLKPGVDYTTITVAVTDSKYDDPISINVRT 94  
 |||||  
 DB 61 GLKPGVDYTTITVAVTDSKYDDPISINVRT 94  
 |||||

RESULT 7  
 ABB78915  
 ID ABB78915 standard; peptide; 94 AA.  
 AC ABB78915;  
 DT 30-JUL-2002 (first entry)  
 XX Tumour necrosis factor-alpha binding amino acid sequence T14.12.  
 DE Protein scaffold; antibody; binding protein; immunoglobulin;  
 KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200232925-A2.  
 XX 25-APR-2002.  
 XX 16-OCT-2001; 2001WO-US032233.  
 XX 16-OCT-2000; 2000US-00688566.  
 XX (PHYL-) PHYLLOS INC.  
 XX Lipovsek D, Wagner RW, Kuimelis RG;  
 XX WPI; 2002-444238/47.  
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CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.4%; Score 486; DB 5; Length 94;

Best Local Similarity 97.9%; Pred. No. 8.7e-49;

Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIIS 60

Db 1 LSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIIS 60

Qy 61 GLKPGVDYITIVYAVTQSDTYKYDDPISINVRT 94

Db 61 GLKPGVDYITIVYAVTQSDTYKYDDPISINVRT 94

RESULT 8

ABB78940

ID ABB78940 standard; peptide; 94 AA.

AC ABB78940;

DT 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence M12.01.

DE Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

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CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
CC not bound as tightly by the reference protein. The non-antibody protein  
CC is useful as scaffolds for selecting or designing a protein framework  
CC with specific and favourable properties, e.g. for binding any antigen of  
CC interest, or for destroying or inactivating antibody molecules. The non-  
CC antibody protein is also useful in all areas where antibodies are used,  
CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
CC binding proteins useful in the above-mentioned fields. The present  
CC proteins have thermodynamic properties superior to those of natural  
CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
CC antibody mimics exhibit improved biophysical properties, such as  
CC stability under reducing conditions and solubility at high  
CC concentrations. In addition, these molecules are readily expressed and  
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention

XX Sequence 94 AA;

Query Match 98.0%; Score 484; DB 5; Length 94;

Best Local Similarity 96.8%; Pred. No. 1.5e-48;

Matches 91; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIIS 60

Db 1 VSDVPRDLEVVAAATPTSLRLISWNRSLQSRYYRITYGTGNSPVQETVPPWASIAIIS 60

Qy 61 GLKPGVDYITIVYAVTQSDTYKYDDPISINVRT 94

Db 61 GLKPGVDYITIVYAVTQSDTYKYDDPISINVRT 94

RESULT 9

ABB78912

ID ABB78912 standard; peptide; 94 AA.

AC ABB78912;

DT 30-JUL-2002 (first entry)

XX Tumour necrosis factor-alpha binding amino acid sequence S08.03.

DE Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework.

XX Homo sapiens.

OS Synthetic.

XX WO200232925-A2.

XX 25-APR-2002.

XX 16-OCT-2001; 2001WO-US032233.

XX 16-OCT-2000; 2000US-00688566.

```
PA (PHYL-) PHYLOS INC.
XX
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
XX domain having an immunoglobulin-like fold, derived from a reference
XX protein having a mutated amino acid sequence, where the non-antibody
XX protein binds with a Kd at least as tight as 10 nM to a compound that is
XX not bound as tightly by the reference protein. The non-antibody protein
XX is useful as scaffolds for selecting or designing a protein framework
XX with specific and favourable properties, e.g. for binding any antigen of
XX interest, or for destroying or inactivating antibody molecules. The non-
XX antibody protein is also useful in all areas where antibodies are used,
XX e.g. research, therapeutic or diagnostic fields, and for screening novel
XX binding proteins useful in the above-mentioned fields. The present
XX proteins have thermodynamic properties superior to those of natural
XX antibodies, and can be evolved rapidly in vitro. The present proteins or
XX antibody mimics exhibit improved biophysical properties, such as
XX concentrations. In addition, these molecules are readily expressed and
XX folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX reticulocyte lysate system). Furthermore, these proteins are extremely
XX amenable to affinity maturation techniques involving multiple cycles of
XX selection, e.g. in vitro selection using RNA-protein fusion technology,
XX phase display or yeast display systems. The present sequence is used in
XX the exemplification of the present invention
XX
XX Sequence 94 AA;
SQ
Query Match 98.0%; Score 484; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 1.5e-48;
Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYGETGNSPVQEFVPPWASATATIS 60
Db 1 VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYGETGNSPVQEFVPPWASATATIS 60
QY 61 GLKPGVDYITIVYAVTMSDITYKDDPISINVRT 94
Db 61 GLKPGVDYITIVYAVTMSDITYKDDPISINVRT 94
RESULT 10
ABE78916
ID ABB78916 standard; peptide; 94 AA.
XX
XX ABB78916;
XX
XX 30-JUL-2002 (first entry)
XX
XX Tumour necrosis factor-alpha binding amino acid sequence T14.13.
XX
XX Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200232925-A2.
XX
XX 25-APR-2002.
XX
XX 16-OCT-2001; 2001WO-US032233.
XX
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XX
XX 16-OCT-2000; 2000US-00688566.
XX (PHYL-) PHYLOS INC.
XX
XX Lipovsek D, Wagner RW, Kuimelis RG;
XX WPI; 2002-444238/47.
XX
XX New non-antibody proteins having an immunoglobulin fold, useful in
XX research, therapeutic or diagnostic fields, particularly as scaffolds for
XX designing proteins with specific properties, e.g. for binding any antigen
XX of interest.
XX
XX Claim 47; Fig 25; 94pp; English.
XX
XX The present invention describes a non-antibody protein, comprising a
XX domain having an immunoglobulin-like fold, derived from a reference
XX protein having a mutated amino acid sequence, where the non-antibody
XX protein binds with a Kd at least as tight as 10 nM to a compound that is
XX not bound as tightly by the reference protein. The non-antibody protein
XX is useful as scaffolds for selecting or designing a protein framework
XX with specific and favourable properties, e.g. for binding any antigen of
XX interest, or for destroying or inactivating antibody molecules. The non-
XX antibody protein is also useful in all areas where antibodies are used,
XX e.g. research, therapeutic or diagnostic fields, and for screening novel
XX binding proteins useful in the above-mentioned fields. The present
XX proteins have thermodynamic properties superior to those of natural
XX antibodies, and can be evolved rapidly in vitro. The present proteins or
XX antibody mimics exhibit improved biophysical properties, such as
XX concentrations. In addition, these molecules are readily expressed and
XX folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX reticulocyte lysate system). Furthermore, these proteins are extremely
XX amenable to affinity maturation techniques involving multiple cycles of
XX selection, e.g. in vitro selection using RNA-protein fusion technology,
XX phase display or yeast display systems. The present sequence is used in
XX the exemplification of the present invention
XX
XX Sequence 94 AA;
SQ
Query Match 97.8%; Score 483; DB 5; Length 94;
Best Local Similarity 97.9%; Pred. No. 1.9e-48;
Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYGETGNSPVQEFVPPWASATATIS 60
Db 1 VSDVPRDLEVVAATPTSLISWNRSGLQSRYYRITYGETGNSPVQELTVPWASATATIS 60
QY 61 GLKPGVDYITIVYAVTMSDITYKDDPISINVRT 94
Db 61 GLKPGVDYITIVYAVTMSDITYKDDPISINVRT 94
RESULT 11
ABE78918
ID ABB78918 standard; peptide; 94 AA.
XX
XX ABB78918;
XX
XX 30-JUL-2002 (first entry)
XX
XX Tumour necrosis factor-alpha binding amino acid sequence T14.05.
XX
XX Protein scaffold; antibody; binding protein; immunoglobulin;
KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX
XX Homo sapiens.
OS Synthetic.
XX
XX WO200232925-A2.
XX
```

PD 25-APR-2002.  
XX 16-OCT-2001; 2001WO-US032233.  
XX 16-OCT-2000; 2000US-00688566.  
XX (PHYL-) PHYLLOS INC.  
XX Lipovsek D, Wagner RW, Kuimelis RG;  
XX WPI; 2002-444238/47.  
XX  
XX New non-antibody proteins having an immunoglobulin fold, useful in  
PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
PT designing proteins with specific properties, e.g. for binding any antigen  
PT of interest.  
XX  
XX Claim 47; Fig 25; 94pp; English.  
XX  
XX The present invention describes a non-antibody protein, comprising a  
CC domain having an immunoglobulin-like fold, derived from a reference  
CC protein having a mutated amino acid sequence, where the non-antibody  
CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
CC not bound as tightly by the reference protein. The non-antibody protein  
CC with specific and favourable properties, e.g. for binding any antigen of  
CC interest, or for destroying or inactivating antibody molecules. The non-  
CC antibody protein is also useful in all areas where antibodies are used,  
CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
CC binding proteins useful in the above-mentioned fields. The present  
CC proteins have thermodynamic properties superior to those of natural  
CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
CC antibody mimics exhibit improved biophysical properties, such as  
CC stability under reducing conditions and solubility at high  
CC concentrations. In addition, these molecules are readily expressed and  
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention  
XX  
XX Sequence 94 AA;  
Query Match 97.8%; Score 483; DB 5; Length 94;  
Best Local Similarity 97.9%; Pred. No. 1.9e-48;  
Matches 92; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYITYGETGNSPVQFTVPWPWASIIATIS 60  
Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYITYGETGNSPVQFTVPWPWASIIATIS 60  
Qy 61 GLKPGVDYITVVAATDKSDTYKYDDPISINRT 94  
Db 61 GLKPGVDYITVVAATDKSDTYKYDDPISINRT 94  
RESULT 12  
ABB78899  
ID ABB78899 standard; peptide; 94 AA.  
XX ABB78899;  
XX  
XX 30-JUL-2002 (first entry)  
XX Tumour necrosis factor-alpha binding amino acid sequence T10.17.  
XX Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework.  
XX Homo sapiens.  
OS Synthetic.

XX WO200232925-A2.  
XX 25-APR-2002.  
XX 16-OCT-2001; 2001WO-US032233.  
XX 16-OCT-2000; 2000US-00688566.  
XX (PHYL-) PHYLLOS INC.  
XX Lipovsek D, Wagner RW, Kuimelis RG;  
XX WPI; 2002-444238/47.  
XX  
XX New non-antibody proteins having an immunoglobulin fold, useful in  
PT research, therapeutic or diagnostic fields, particularly as scaffolds for  
PT designing proteins with specific properties, e.g. for binding any antigen  
PT of interest.  
XX  
XX Claim 47; Fig 25; 94pp; English.  
XX  
XX The present invention describes a non-antibody protein, comprising a  
CC domain having an immunoglobulin-like fold, derived from a reference  
CC protein having a mutated amino acid sequence, where the non-antibody  
CC protein binds with a Kd at least as tight as 10 nM to a compound that is  
CC not bound as tightly by the reference protein. The non-antibody protein  
CC is useful as scaffolds for selecting or designing a protein framework  
CC with specific and favourable properties, e.g. for binding any antigen of  
CC interest, or for destroying or inactivating antibody molecules. The non-  
CC antibody protein is also useful in all areas where antibodies are used,  
CC e.g. research, therapeutic or diagnostic fields, and for screening novel  
CC binding proteins useful in the above-mentioned fields. The present  
CC proteins have thermodynamic properties superior to those of natural  
CC antibodies, and can be evolved rapidly in vitro. The present proteins or  
CC antibody mimics exhibit improved biophysical properties, such as  
CC stability under reducing conditions and solubility at high  
CC concentrations. In addition, these molecules are readily expressed and  
CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic  
CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit  
CC reticulocyte lysate system). Furthermore, these proteins are extremely  
CC amenable to affinity maturation techniques involving multiple cycles of  
CC selection, e.g. in vitro selection using RNA-protein fusion technology,  
CC phage display or yeast display systems. The present sequence is used in  
CC the exemplification of the present invention  
XX  
XX Sequence 94 AA;  
Query Match 97.4%; Score 481; DB 5; Length 94;  
Best Local Similarity 98.9%; Pred. No. 3.3e-48;  
Matches 93; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYITYGETGNSPVQFTVPWPWASIIATIS 60  
Db 1 VSDVPRDLEVVAAATPTSLISWNRSGLQSYRYITYGETGNSPVQFTVPWPWASIIATIS 60  
Qy 61 GLKPGVDYITVVAATDKSDTYKYDDPISINRT 94  
Db 61 GLKPGVDYITVVAATDKSDTYKYDDPISINRT 94  
RESULT 13  
ABB78917  
ID ABB78917 standard; peptide; 94 AA.  
XX ABB78917;  
XX  
XX 30-JUL-2002 (first entry)  
XX Tumour necrosis factor-alpha binding amino acid sequence T14.17.  
XX Protein scaffold; antibody; binding protein; immunoglobulin;  
KW tumour necrosis factor alpha; TNF-alpha; protein framework.

```

XX OS Homo sapiens.
XX KW Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WIPI; 2002-444238/47.
XX DR New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
XX Query Match 96.8%; Score 478; DB 5; Length 94;
XX Best Local Similarity 97.9%; Pred. No. 7.5e-48;
XX Matches 92; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX QY 1 VSDVPRDLEVVAATPTSLRSLISWNRSLQSRVYRITYGTGGNSPVQEFVTPPWASITATIS 60
XX Db 1 VSDVPRGLEVVAATPTSLRSLISWNRSLQSRVYRITYGTGGNSPVQEFVTPPWASITATIS 60
XX QY 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINVRT 94
XX Db 61 GLKHGVDYITIVYAVTDKSDTYKYDDPISINVRT 94
XX RESULT 14
XX ABB78922
XX ID ABB78922 standard; peptide; 94 AA.
XX AC ABB78922;
XX XX 30-JUL-2002 (first entry)
XX DT Tumour necrosis factor-alpha binding amino acid sequence T14.24.
XX DE

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```

XX KW Protein scaffold; antibody; binding protein; immunoglobulin;
XX KW tumour necrosis factor alpha; TNF-alpha; protein framework.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200232925-A2.
XX PD 25-APR-2002.
XX PF 16-OCT-2001; 2001WO-US032233.
XX PR 16-OCT-2000; 2000US-00688566.
XX PA (PHYL-) PHYLOS INC.
XX PI Lipovsek D, Wagner RW, Kuimelis RG;
XX WIPI; 2002-444238/47.
XX DR New non-antibody proteins having an immunoglobulin fold, useful in
XX PT research, therapeutic or diagnostic fields, particularly as scaffolds for
XX PT designing proteins with specific properties, e.g. for binding any antigen
XX PT of interest.
XX PS Claim 47; Fig 25; 94pp; English.
XX CC The present invention describes a non-antibody protein, comprising a
XX CC domain having an immunoglobulin-like fold, derived from a reference
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody
XX CC protein binds with a Kd at least as tight as 10 nM to a compound that is
XX CC not bound as tightly by the reference protein. The non-antibody protein
XX CC is useful as scaffolds for selecting or designing a protein framework
XX CC with specific and favourable properties, e.g. for binding any antigen of
XX CC interest, or for destroying or inactivating antibody molecules. The non-
XX CC antibody protein is also useful in all areas where antibodies are used,
XX CC e.g. research, therapeutic or diagnostic fields, and for screening novel
XX CC binding proteins useful in the above-mentioned fields. The present
XX CC proteins have thermodynamic properties superior to those of natural
XX CC antibodies, and can be evolved rapidly in vitro. The present proteins or
XX CC stability under reducing conditions and solubility at high
XX CC concentrations. In addition, these molecules are readily expressed and
XX CC folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic
XX CC systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit
XX CC reticulocyte lysate system). Furthermore, these proteins are extremely
XX CC amenable to affinity maturation techniques involving multiple cycles of
XX CC selection, e.g. in vitro selection using RNA-protein fusion technology,
XX CC phage display or yeast display systems. The present sequence is used in
XX CC the exemplification of the present invention
XX SQ Sequence 94 AA;
XX Query Match 93.7%; Score 463; DB 5; Length 94;
XX Best Local Similarity 93.6%; Pred. No. 4.3e-46;
XX Matches 88; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX QY 1 VSDVPRDLEVVAATPTSLRSLISWNRSLQSRVYRITYGTGGNSPVQEFVTPPWASITATIS 60
XX Db 1 VSDVPRDLEVVAATPTSLRSLISWNRSLQSRVYRITYGTGGNSPVQEFVTPPWASITATIS 60
XX QY 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINVRT 94
XX Db 61 GLKPGVDYITIVYAVTDKSDTYKYDDPISINVRT 94
XX RESULT 15
XX ABB78923
XX ID ABB78923 standard; peptide; 94 AA.
XX AC ABB78923;
XX XX
XX XX

```



DT	30-JUL-2002	(first entry)	
XX			
XX		Tumour necrosis factor-alpha binding amino acid sequence T14.20.	
XX			
KW		Protein scaffold; antibody; binding protein; immunoglobulin;	
KW		tumour necrosis factor alpha; TNF-alpha; protein framework.	
XX			
OS		Homo sapiens.	
OS		Synthetic.	
PN	WO200232925-A2.		
PD			
XX	25-APR-2002.		
XX			
PF	16-OCT-2001; 2001WO-US032233.		
XX			
PR	16-OCT-2000; 2000US-00688566.		
XX	(PHYL-) PHYLOS INC.		
XX			
PI	Lipovsek D, Wagner RW, Kuimelis RG;		
XX			
DR	WFI; 2002-444238/47.		
XX			
PS	Claim 47; Fig 25; 94pp; English.		
XX			
CC	The present invention describes a non-antibody protein, comprising a		
CC	domain having an immunoglobulin-like fold, derived from a reference		
CC	protein having a mutated amino acid sequence, where the non-antibody		
CC	protein binds with a Kd at least as tight as 10 nM to a compound that is		
CC	not bound as tightly by the reference protein. The non-antibody protein		
CC	is useful as scaffolds for selecting or designing a protein framework		
CC	with specific and favourable properties, e.g. for binding any antigen of		
CC	interest, or for destroying or inactivating antibody molecules. The non-		
CC	antibody protein is also useful in all areas where antibodies are used,		
CC	e.g. research, therapeutic or diagnostic fields, and for screening novel		
CC	binding proteins useful in the above-mentioned fields. The present		
CC	inventions have thermodynamic properties superior to those of natural		
CC	antibodies, and can be evolved rapidly in vitro. The present proteins or		
CC	antibody mimics exhibit improved biophysical properties, such as		
CC	stability under reducing conditions and solubility at high		
CC	concentrations. In addition, these molecules are readily expressed and		
CC	folded in prokaryotic systems (e.g. Escherichia coli), in eukaryotic		
CC	systems (e.g. yeast), or in in vitro translation systems (e.g. rabbit		
CC	reticulocyte lysate system). Furthermore, these proteins are extremely		
CC	amenable to affinity maturation techniques involving multiple cycles of		
CC	selection, e.g. in vitro selection using RNA-protein fusion technology,		
CC	phage display or yeast display systems. The present sequence is used in		
CC	the exemplification of the present invention		
XX			
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	Query Match	90.3%;	Score 446; DB 5; Length 94;
	Best Local Similarity	94.5%;	Pred. No. 4.2e-44;
	Matches 86; Conservative 1;	Mismatches 7;	Indels 0; Gaps 0
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DB	1	VSDVPRDLEVVAAAPTSELISWRNIYPIARYRITYGTGGNSPVQETVTPPWASIAIIS	60
QY	61	GLKPGVDYITIVYAVTDKSDTKYKDDPISINVRT	94
DB	61	GLKPGADYITIVYAVTDKSDTKYKDDPISINVRT	94

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Job time : 165 secs

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OM protein - protein search, using sw model

Run on: May 18, 2005, 14:57:44 ; Search time 43 Seconds  
(without alignments)  
163.186 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDPRDLVVAAATPTSLRI.....VTDKSDTYKYDDPISINYRT 94

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	361	73.1	94	US-08-717-169-8	Sequence 8, Appl
2	361	73.1	94	US-09-638-202A-110	Sequence 110, App
3	361	73.1	94	US-09-228-901A-8	Sequence 8, Appl
4	361	73.1	94	US-09-096-749A-110	Sequence 110, App
5	361	73.1	94	US-09-637-614-110	Sequence 110, App
6	361	73.1	96	US-09-638-202A-112	Sequence 112, App
7	361	73.1	96	US-09-096-749A-112	Sequence 112, App
8	361	73.1	96	US-09-637-614-112	Sequence 112, App
9	361	73.1	175	US-08-078-683A-34	Sequence 34, Appl
10	361	73.1	175	US-08-471-970A-34	Sequence 34, Appl
11	361	73.1	175	US-09-723-677B-34	Sequence 34, Appl
12	361	73.1	256	US-07-959-369-1	Sequence 1, Appl
13	361	73.1	258	US-07-959-369-10	Sequence 10, Appl
14	361	73.1	274	US-07-959-369-12	Sequence 12, Appl
15	361	73.1	274	US-08-836-854-3	Sequence 3, Appl
16	361	73.1	274	US-09-366-009-25	Sequence 25, Appl
17	361	73.1	274	US-08-809-156B-25	Sequence 25, Appl
18	361	73.1	277	US-07-959-369-3	Sequence 3, Appl
19	361	73.1	279	US-07-959-369-11	Sequence 11, Appl
20	361	73.1	279	US-08-836-854-8	Sequence 8, Appl
21	361	73.1	281	US-07-959-369-4	Sequence 4, Appl
22	361	73.1	283	US-07-959-369-13	Sequence 13, Appl
23	361	73.1	283	US-08-836-854-7	Sequence 7, Appl
24	361	73.1	302	US-08-836-854-5	Sequence 5, Appl
25	361	73.1	302	US-09-366-009-29	Sequence 29, Appl
26	361	73.1	302	US-08-809-156B-29	Sequence 29, Appl
27	361	73.1	332	US-08-836-854-13	Sequence 13, Appl

28	361	73.1	341	2	US-08-836-854-14	Sequence 14, Appl
29	361	73.1	367	2	US-08-836-854-18	Sequence 18, Appl
30	361	73.1	368	2	US-08-836-854-17	Sequence 17, Appl
31	361	73.1	383	1	US-07-959-369-5	Sequence 5, Appl
32	361	73.1	385	1	US-07-959-369-14	Sequence 14, Appl
33	361	73.1	385	2	US-08-836-854-10	Sequence 10, Appl
34	361	73.1	422	2	US-08-836-854-12	Sequence 12, Appl
35	361	73.1	432	1	US-07-959-369-8	Sequence 8, Appl
36	361	73.1	432	1	US-07-959-369-9	Sequence 9, Appl
37	361	73.1	432	2	US-08-836-854-20	Sequence 20, Appl
38	361	73.1	432	4	US-09-366-009-4	Sequence 4, Appl
39	361	73.1	432	4	US-08-809-156B-4	Sequence 4, Appl
40	361	73.1	446	2	US-08-836-854-15	Sequence 15, Appl
41	361	73.1	457	2	US-08-836-854-16	Sequence 16, Appl
42	361	73.1	457	4	US-09-366-009-5	Sequence 5, Appl
43	361	73.1	457	4	US-09-366-009-22	Sequence 22, Appl
44	361	73.1	457	4	US-08-809-156B-5	Sequence 5, Appl
45	361	73.1	457	4	US-08-809-156B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1  
US-08-717-169-8  
; Sequence 8, Application US/08717169  
; Patent No. 5922676  
; GENERAL INFORMATION:  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Ruoslahti, Erkki  
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and  
; TITLE OF INVENTION: Ameliorating Cancer By Using Superfibronection  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA: US/08/717,169  
; APPLICATION NUMBER: US/08/717,169  
; FILING DATE: 20-SEP-1996  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-LJ 2017  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-717-169-8

Query Match 73.1%; Score 361; DB 2; Length 94;  
Best Local Similarity 77.7%; Pred. No. 1.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDPRDLVVAAATPTSLRI...VTDKSDTYKYDDPISINYRT 60  
|||||  
Db 1 VSDPRDLVVAAATPTSLRI...VTDKSDTYKYDDPISINYRT 60  
|||||

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QY 61 GLKPGVDYITVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITVAVTGRGDSPASSKPIINVRT 94

RESULT 2
US-09-638-202A-110
; Sequence 110, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-AUG-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-638-202A-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLIWNRSGLQSYRYITYGETGNSPVQEFVTPPWASITATIS 60
      |||||
Db 1 VSDVPRDLVVAATPTSLIWNDAFVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 60

QY 61 GLKPGVDYITVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITVAVTGRGDSPASSKPIINVRT 94

RESULT 4
US-09-096-749A-110
; Sequence 110, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749A
; FILING DATE: June 12, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 94 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-096-749A-110

Query Match 73.1%; Score 361; DB 4; Length 94;
Best Local Similarity 77.7%; Pred. No. 1.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLIWNRSGLQSYRYITYGETGNSPVQEFVTPPWASITATIS 60
      |||||
Db 1 VSDVPRDLVVAATPTSLIWNDAFVTVRYRYITYGETGNSPVQEFVTPGSKSTATIS 60

QY 61 GLKPGVDYITVAVTKSDTYKYDDPISINVRT 94
      |||||
Db 61 GLKPGVDYITVAVTGRGDSPASSKPIINVRT 94

RESULT 3
US-09-228-901A-8
; Sequence 8, Application US/09228901A
; Patent No. 6475488
; GENERAL INFORMATION:
; APPLICANT: Pasqualini, Renata
; APPLICANT: Ruoslahti, Erkki I.
; TITLE OF INVENTION: Methods of Inhibiting Angiogenesis and
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<b>Query Match</b>	73.1%	<b>Score</b> 361;	<b>DB</b> 4;	<b>Length</b> 94;
<b>Best Local Similarity</b>	77.7%;	<b>Pred. No.</b> 1.9e-35;		
<b>Matches</b> 73; Conservative	4;	<b>Mismatches</b> 17;	<b>Indels</b> 0;	<b>Gaps</b> 0;

  

<b>QY</b>	1	VSDVPRDLVVAATPSRLISWNRSGLOQSRYRITYGETGNSPVQSEFTVPPIASITATIS	60
		:	
<b>Db</b>	1	VSDVPRDLVVAATPSLLISWDAPAVTVRYRITYGETGNSPVQSEFTVPFSKSTATIS	60
		:	
<b>QY</b>	61	GLKPGVDYTTIVAAVTDKSDTYKYDDPISINRYT	94
		:	
<b>Db</b>	61	GLKPGVDYTTIVAAVTGRGDSPASSKPEISINRYT	94
		:	

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RESULT 6
US-09-638-202A-112
; Sequence 112, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensine
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-09-638-202A-112

Query Match      73.1%; Score 361; DB 4; Length 96;
Best Local Similarity 77.7%; Pred. No. 2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0

QY      1 VSDVPRLDLEVAATPSRLISWMNRSGIQSRYRITYGETGNSPVQFTVPPWASIIATIS 60
        |||||
Db       3 VSDVPRLDLEVAATPSLLISWDAPAVTVRYRITYGETGNSPVQFTVPGSKSTATIS 62
        |||||

QY      61 GLKPGVDYITIVAVTGDKSDTYKYDDPISINYRT 94
        |||||
Db       63 GLKPGVDYITIVAVTGRGDSPASSKPISINYRT 96
        |||||

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RESULT 7
US-09-096-749A-112
; Sequence 112, Application US/09096749A
; Patent No. 6673901
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
;

```



FRAGMENT TYPE: internal  
US-08-078-683A-34

Query Match 73.1%; Score 361; DB 1; Length 175;  
Best Local Similarity 77.7%; Pred. No. 4.4e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
  
Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 141  
  
Qy 61 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 94  
Db 142 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 175

RESULT 10  
US-08-471-970A-34  
; Sequence 34, Application US/08471970A  
; Patent No. 6531295  
; GENERAL INFORMATION:  
; APPLICANT: Saunders, Scott  
; APPLICANT: Bernfield, Merton  
; APPLICANT: Kato, Masato  
; TITLE OF INVENTION: Construction and Use of Synthetic  
; TITLE OF INVENTION: Constructs Encoding Syndecan  
; NUMBER OF SEQUENCES: 45  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LAHIVE & COCKFIELD  
; STREET: 28 State Street  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: ASCII (text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/471,970A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/078,683  
; FILING DATE: 17-JUN-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kara, Catherine J.  
; REGISTRATION NUMBER: P-41,106  
; REFERENCE/DOCKET NUMBER: CME-062DV  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 227-7400  
; TELEFAX: (617) 227-5941  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 175 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal  
; US-08-471-970A-34

Query Match 73.1%; Score 361; DB 4; Length 175;  
Best Local Similarity 77.7%; Pred. No. 4.4e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
  
Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 141  
  
Qy 61 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 94  
Db 142 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 175

## RESULT 11

US-09-723-677B-34  
; Sequence 34, Application US/09723677B  
; Patent No. 6699968  
; GENERAL INFORMATION:  
; APPLICANT: SAUNDERS, SCOTT  
; APPLICANT: BERNFIELD, MERTON  
; APPLICANT: KATO, MASATO  
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN  
; FILE REFERENCE: 101353-151  
; CURRENT APPLICATION NUMBER: US/09/723,677B  
; CURRENT FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 08/471,970  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/078,683  
; PRIOR FILING DATE: 1993-06-17  
; PRIOR APPLICATION NUMBER: 07/856,869  
; PRIOR FILING DATE: 1992-03-24  
; PRIOR APPLICATION NUMBER: 07/757,654  
; PRIOR FILING DATE: 1991-09-06  
; PRIOR APPLICATION NUMBER: 07/746,797  
; PRIOR FILING DATE: 1991-08-12  
; PRIOR APPLICATION NUMBER: 07/331,585  
; PRIOR FILING DATE: 1989-03-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: Patent In version 3.0  
; SEQ ID NO 34  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: MUS SP;HOMO SAPIEN  
US-09-723-677B-34

Query Match 73.1%; Score 361; DB 4; Length 175;

Best Local Similarity 77.7%; Pred. No. 4.4e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 60  
Db 82 VSDVPRDLEVAATPTSLISWNSGLQSRYYRITYGETGNSPVQETVPPWASIIATIS 141  
  
Qy 61 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 94  
Db 142 GLKPGVDYITVYAVTKSDTKYKDDPISINRYT 175

## RESULT 12

US-07-959-369-1  
; Sequence 1, Application US/07959369  
; Patent No. 5302701  
; GENERAL INFORMATION:  
; APPLICANT: Hidetaka HASHI et al.  
; TITLE OF INVENTION: No. 5302701e1 Functional Polypeptide  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wenderoth, Lind & Ponack  
; STREET: 805 Fifteenth Street, N.W., #700  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: Wordperfect 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/959,369  
; FILING DATE: 19921013  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 256 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
; US-07-959-369-1

Query Match 73.1%; Score 361; DB 1; Length 256;
Best Local Similarity 77.7%; Pred. No. 7.2e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLVVAATPTSLISMNRSGLQSRYYRITYGETGNSPVQVEFTVPPWASIAIIS 60
Db 157 VSDVPRDLVVAATPTSLISWDPAPVTVYYRITYGETGNSPVQVEFTVPGSKSTATIS 216

QY 61 GLKPGVDYITTVYAVTKSDTYKYDDPISINYRT 94
Db 217 GLKPGVDYITTVYAVTGRGDSPASSKPIISINYRT 250

RESULT 13
US-07-959-369-10
; Sequence 10, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 258 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:
; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:

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; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-10
Query Match 73.1%; Score 361; DB 1; Length 258;
Best Local Similarity 77.7%; Pred. No. 7.3e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRYITYGETGNSPVQBEFTVPWASIATIS 60
Db 157 VSDVPRDLEVVAAATPTSLISWDAVAVTVYRYITYGETGNSPVQBEFTVPGSKSTATIS 216

Qy 61 GLKPGVDYTTITVAATDKSDTKYDDPISINVRT 94
Db 217 GLKPGVDYTTITVAATGGRDGPASSKPIISINVRT 250

RESULT 14
US-07-959-369-12
; Sequence 12, Application US/07959369
; Patent No. 5302701
; GENERAL INFORMATION:
; APPLICANT: Hidetaka HASHI et al.
; TITLE OF INVENTION: No. 5302701el Functional Polypeptide
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/959,369
; FILING DATE: 19921013
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 274 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; HYPOTHETICAL:
; ANTI-SENSE:
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM:
; STRAIN:
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE:
; HAPLOTYPE:
; TISSUE TYPE:
; CELL TYPE:
; CELL LINE:
; ORGANELLE:
; IMMEDIATE SOURCE:
; LIBRARY:

; CLONE:
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT:
; MAP POSITION:
; UNITS:
; FEATURE:
; NAME/KEY:
; LOCATION:
; IDENTIFICATION METHOD:
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; AUTHORS:
; TITLE:
; JOURNAL:
; VOLUME:
; ISSUE:
; PAGES:
; DATE:
; DOCUMENT NUMBER:
; FILING DATE:
; PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-959-369-12
Query Match 73.1%; Score 361; DB 1; Length 274;
Best Local Similarity 77.7%; Pred. No. 7.9e-35;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLISWNRSGLSQRYRYITYGETGNSPVQBEFTVPWASIATIS 60
Db 178 VSDVPRDLEVVAAATPTSLISWDAVAVTVYRYITYGETGNSPVQBEFTVPGSKSTATIS 237

Qy 61 GLKPGVDYTTITVAATDKSDTKYDDPISINVRT 94
Db 238 GLKPGVDYTTITVAATGGRDGPASSKPIISINVRT 271

RESULT 15
US-08-836-854-3
; Sequence 3, Application US/08836854
; Patent No. 5824547
; GENERAL INFORMATION:
; APPLICANT: HASHINO, Kimikazu
; APPLICANT: MATSUSHITA, Hideyuki
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: METHOD OF PRODUCTION OF TRANSFECTED CELLS
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh Street N.W. Ste. 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,854
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/02425
; FILING DATE: 29-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 317721/1994
; FILING DATE: 29-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Browdy, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: HASHINO=1
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; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 274 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-836-854-3

Query Match 73.1%; Score 361; DB 2; Length 274;  
Best Local Similarity 77.7%; Pred. No. 7.9e-35;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
  
QY 1 VSDVPRDLEVVAATPTSLRLISWNRGLQSRYYRITYGETGNSPVQEFVPPWASIIATIS 60  
Db 178 VSDVPRDLEVVAATPTSLRLISWNRGLQSRYYRITYGETGNSPVQEFVPPWASIIATIS 237  
  
QY 61 GLKPGVDYITIVYAVTGRGDSPPASSKXPISINVRT 94  
Db 238 GLKPGVDYITIVYAVTGRGDSPPASSKXPISINVRT 271

Search completed: May 18, 2005, 15:31:48  
Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2005, 15:35:03 ; Search time 134 Seconds  
(without alignments)  
234.655 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVPRDLEVVAAVTSRLI.....VTDKSDTYKYDDPISINVRT 94

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1434725 seqs, 334507595 residues

Total number of hits satisfying chosen parameters: 1434725

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367.5	74.4	96	14	US-10-302-456-1
2	361	73.1	94	9	US-09-096-749A-110
3	361	73.1	94	14	US-10-174-717A-110
4	361	73.1	94	14	US-10-165-155-110
5	361	73.1	94	14	US-10-190-162-110
6	361	73.1	96	9	US-09-096-749A-112
7	361	73.1	96	10	US-09-903-412-110
8	361	73.1	96	10	US-09-903-412-112
9	361	73.1	96	10	US-09-903-412-121
10	361	73.1	96	14	US-10-174-717A-112
11	361	73.1	96	14	US-10-165-155-112
12	361	73.1	96	14	US-10-190-162-112
13	361	73.1	96	14	US-10-006-760-2

14	361	73.1	175	17	US-10-776-989-34	Sequence 34, Appl
15	361	73.1	274	10	US-09-775-964-25	Sequence 25, Appl
16	361	73.1	274	17	US-10-486-512-1	Sequence 1, Appl
17	361	73.1	302	17	US-09-775-964-29	Sequence 29, Appl
18	361	73.1	302	17	US-10-486-512-7	Sequence 7, Appl
19	361	73.1	330	14	US-10-279-733-10	Sequence 10, Appl
20	361	73.1	367	17	US-10-486-512-8	Sequence 8, Appl
21	361	73.1	368	17	US-10-486-512-9	Sequence 9, Appl
22	361	73.1	370	17	US-10-486-512-10	Sequence 10, Appl
23	361	73.1	432	10	US-09-775-964-4	Sequence 4, Appl
24	361	73.1	457	10	US-09-775-964-5	Sequence 5, Appl
25	361	73.1	457	10	US-09-775-964-22	Sequence 22, Appl
26	361	73.1	457	17	US-10-486-512-11	Sequence 11, Appl
27	361	73.1	464	10	US-09-775-964-7	Sequence 7, Appl
28	361	73.1	472	10	US-09-775-964-21	Sequence 21, Appl
29	361	73.1	472	17	US-10-486-512-12	Sequence 12, Appl
30	361	73.1	489	10	US-09-775-964-8	Sequence 8, Appl
31	361	73.1	549	10	US-09-775-964-23	Sequence 23, Appl
32	361	73.1	549	17	US-10-486-512-5	Sequence 5, Appl
33	361	73.1	574	10	US-09-775-964-24	Sequence 24, Appl
34	361	73.1	574	17	US-10-486-512-6	Sequence 6, Appl
35	361	73.1	599	14	US-10-279-733-9	Sequence 9, Appl
36	361	73.1	826	10	US-09-775-964-14	Sequence 14, Appl
37	361	73.1	847	16	US-10-741-601-361	Sequence 361, Appl
38	361	73.1	847	17	US-10-741-600-1073	Sequence 1073, Ap
39	361	73.1	1259	16	US-10-741-601-365	Sequence 365, App
40	361	73.1	1259	17	US-10-741-600-1077	Sequence 1077, Ap
41	361	73.1	1286	16	US-10-741-601-362	Sequence 362, App
42	361	73.1	1286	17	US-10-741-600-1074	Sequence 1074, Ap
43	361	73.1	1315	16	US-10-741-601-358	Sequence 358, App
44	361	73.1	1315	17	US-10-741-600-1068	Sequence 1068, App
45	361	73.1	1341	16	US-10-741-601-355	Sequence 355, App

ALIGNMENTS

RESULT 1  
US-10-302-456-1  
; Sequence 1, Application US/10302456  
; Publication No. US20030100004A1  
; GENERAL INFORMATION:  
; APPLICANT: Kurz, Markus  
; TITLE OF INVENTION: Solid Phase Immobilization of Proteins  
; TITLE OF INVENTION: and Peptides  
; FILE REFERENCE: 50036/051002  
; CURRENT APPLICATION NUMBER: US/10/302,456  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 60/333,470  
; PRIOR FILING DATE: 2001-11-27  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-302-456-1

Query Match 74.4%; Score 367.5; DB 14; Length 96;  
Best Local Similarity 80.0%; Pred. No. 4.5e-34;  
Matches 76; Conservative 3; Mismatches 15; Indels 1; Gaps 1;

Qy	1	VSDVPRDLEVVAAVTSRLISWNSGLQSVYRITYGETGNSPVQETVPWASIAIS 60
Db	2	VSDVPRDLEVVAAVTSRLISWNSGLQSVYRITYGETGNSPVQETVPWASIAIS 61
Qy	61	GLKPGVDYTTVAVTDKSDT-VKYDDPISINVRT 94
Db	62	GLKPGVDYTTVAVTPIRWTEAHIPINVRT 96

RESULT 2  
US-09-096-749A-110  
; Sequence 110, Application US/09096749A  
; Patent No. US20020019517A1  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749A  
; FILING DATE: June 12, 1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; FILING DATE:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; US-09-096-749A-110

Query Match 73.1%; Score 361; DB 9; Length 94;  
Best Local Similarity 77.7%; Pred. No. 2.4e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGGNSPVQOEFTVPPWASTATIS 60  
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGGNSPVQOEFTVPPWASTATIS 60  
QY 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINVRT 94  
Db 61 GLKPGVDYITVYAVTGRGDSPASSKPIINVRT 94

RESULT 3  
US-10-174-717A-110  
; Sequence 110, Application US/10174717A  
; Publication No. US20030108948A1  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, St. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: WINDOWS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/174,717A  
; FILING DATE: 18-Jun-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/096,749  
; FILING DATE: June 12, 1998  
; APPLICATION NUMBER: 60/049,410  
; FILING DATE: June 12, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ann S. Viksnins  
; REGISTRATION NUMBER: 37,748  
; REFERENCE/DOCKET NUMBER: 109.034US4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (612) 373-6900  
; TELEFAX: (612) 339-3061  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 94 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: internal  
; ORIGINAL SOURCE:  
; SEQUENCE DESCRIPTION: SEQ ID NO: 110:  
US-10-174-717A-110  
Query Match 73.1%; Score 361; DB 14; Length 94;  
Best Local Similarity 77.7%; Pred. No. 2.4e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGGNSPVQOEFTVPPWASTATIS 60  
Db 1 VSDVPRDLEVAATPTSLISWNRSLQSRYYRITYGETGGNSPVQOEFTVPPWASTATIS 60  
QY 61 GLKPGVDYITVYAVTDKSDTYKYDDPISINVRT 94  
Db 61 GLKPGVDYITVYAVTGRGDSPASSKPIINVRT 94  
RESULT 4  
US-10-165-155-110  
; Sequence 110, Application US/10165155  
; Publication No. US20030134386A1  
; GENERAL INFORMATION:  
; APPLICANT: Koleda, Shohel  
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES  
; NUMBER OF SEQUENCES: 118  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.  
; STREET: 121 South Eighth Street, Ste. 1600  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/165,155  
; FILING DATE: 06-Jun-2002  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/096,749  
; FILING DATE: June 12, 1998

1	VSDVPRDLVVAAATPTSRLLISNRSLQSLRYRITYITGETGGNSPVQERTVPWASIAITIS	60
Qy		
STRANDEDNESS: single		
TOPOLOGY: linear		

Db 3 VSDVPRDLEVAATPTSLISWDAPAVTVYYRITYGETGNSPVQEFVTPGSKSTATIS 62

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94  
|||||:|:|

Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINVRT 96  
|||||:|:|

RESULT 7

US-09-903-412-110

; Sequence 110, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 110

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The synthetic Fn3 gene.

US-09-903-412-110

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
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Db 3 VSDVPRDLEVAATPTSLISWDAPAVTVYYRITYGETGNSPVQEFVTPGSKSTATIS 62  
|||||:|:|

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94  
|||||:|:|

Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINVRT 96  
|||||:|:|

RESULT 8

US-09-903-412-112

; Sequence 112, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; PRIOR FILING DATE: 2000-07-11

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 112

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: The designed Fn3 gene.

US-09-903-412-112

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
|||||:|:|

Db 3 VSDVPRDLEVAATPTSLISWDAPAVTVYYRITYGETGNSPVQEFVTPGSKSTATIS 62  
|||||:|:|

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94  
|||||:|:|

Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINVRT 96  
|||||:|:|

RESULT 9

US-09-903-412-121

; Sequence 121, Application US/09903412

; Publication No. US20030027319A1

; GENERAL INFORMATION:

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; FILE REFERENCE: 109.050US1

; CURRENT APPLICATION NUMBER: US/09/903,412

; CURRENT FILING DATE: 2001-07-11

; PRIOR FILING DATE: 2000-07-11

; PRIOR APPLICATION NUMBER: US 60/217,474

; NUMBER OF SEQ ID NOS: 121

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 121

; LENGTH: 96

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-903-412-121

Query Match 73.1%; Score 361; DB 10; Length 96;

Best Local Similarity 77.7%; Pred. No. 2.5e-33;

Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSLQSRYYRITYGETGNSPVQEFVTPPWASITATIS 60  
|||||:|:|

Db 3 VSDVPRDLEVAATPTSLISWDAPAVTVYYRITYGETGNSPVQEFVTPGSKSTATIS 62  
|||||:|:|

QY 61 GLKPGVDYITTVAVTDKSDTYKYDDPISINVRT 94  
|||||:|:|

Db 63 GLKPGVDYITTVAVTGRGDSPASSKPISINVRT 96  
|||||:|:|

RESULT 10

US-10-174-717A-112

; Sequence 112, Application US/10174717A

; Publication No. US20030108948A1

; APPLICANT: Koide, Shohei

; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES

; NUMBER OF SEQUENCES: 118

; CORRESPONDENCE ADDRESS:

; ADDRESS: Schwegman, Lundberg, Woessner & Kluth P.A.

; STREET: 121 South Eighth Street, St. 1600

; CITY: Minneapolis

; STATE: MN

; COUNTRY: USA

; ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: WINDOWS

SOFTWARE: FastSeq Version 2.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/174,717A

FILING DATE: 18-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/096,749

FILING DATE: June 12, 1998

APPLICATION NUMBER: 60/049,410

FILING DATE: June 12, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ann S. Viksnins

REGISTRATION NUMBER: 37,748

REFERENCE/DOCKET NUMBER: 109.034US4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (612) 373-6900

TELEFAX: (612) 339-3061

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

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; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-174-717A-112

Query Match          73.1%; Score 361; DB 14; Length 96;
Best Local Similarity 77.7%; Pred. No. 2.5e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRSLISWNRSGLSQRYRITYGETGGNSPVQVEFTVPPWASIATIS 60
Db 3 VSDVPRDLEVVAAATPTSLRSLISWDAVAVTVRYRITYGETGGNSPVQVEFTVPGSKSTATIS 62

Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
Db 63 GLKPGVDYTIIVYAVTGRGDSPASSKPISINVRT 96

RESULT 11
US-10-165-155-112
; Sequence 112, Application US/10165155
; Publication No. US20030134386A1
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/165,155
; FILING DATE: 06-Jun-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-165-155-112

Query Match          73.1%; Score 361; DB 14; Length 96;
Best Local Similarity 77.7%; Pred. No. 2.5e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRSLISWNRSGLSQRYRITYGETGGNSPVQVEFTVPPWASIATIS 60
Db 3 VSDVPRDLEVVAAATPTSLRSLISWDAVAVTVRYRITYGETGGNSPVQVEFTVPGSKSTATIS 62

Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
Db 63 GLKPGVDYTIIVYAVTGRGDSPASSKPISINVRT 96

US-10-165-155-112
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Query Match

73.1%; Score 361; DB 14; Length 96;

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Best Local Similarity 77.7%; Pred. No. 2.5e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRSLISWNRSGLSQRYRITYGETGGNSPVQVEFTVPPWASIATIS 60
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Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
Db 63 GLKPGVDYTIIVYAVTGRGDSPASSKPISINVRT 96

RESULT 12
US-10-190-162-112
; Sequence 112, Application US/10190162
; Publication No. US20030170753A1
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/190,162
; FILING DATE: 03-Jul-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,749
; FILING DATE: June 12, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Vikensins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-190-162-112

Query Match          73.1%; Score 361; DB 14; Length 96;
Best Local Similarity 77.7%; Pred. No. 2.5e-33;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLEVVAAATPTSLRSLISWNRSGLSQRYRITYGETGGNSPVQVEFTVPPWASIATIS 60
Db 3 VSDVPRDLEVVAAATPTSLRSLISWDAVAVTVRYRITYGETGGNSPVQVEFTVPGSKSTATIS 62

Qy 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
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RESULT 13
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US-10-006-760-2  
; Sequence 2, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohel  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/249,756  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 96  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-006-760-2

Query Match 73.1%; Score 361; DB 14; Length 96;  
Best Local Similarity 77.7%; Pred. No. 2.5e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVVAATPTSLISWDAAPVTVYRYITYGETGNSPVQEFVPPWASITATIS 60  
Db 3 VSDVPRDLEVVAATPTSLISWDAAPVTVYRYITYGETGNSPVQEFVPPWASITATIS 62  
QY 61 GLKPGVDYITVYAVTSDTKSDTYKYDDPISINVRT 94  
Db 63 GLKPGVDYITVYAVTGRGDSPPASSKPSISINVRT 96

RESULT 14  
US-10-776-989-34  
; Sequence 34, Application US/10776989  
; Publication No. US20050075484A1  
; GENERAL INFORMATION:  
; APPLICANT: SAUNDERS, SCOTT  
; APPLICANT: BERNFIELD, MERTON  
; APPLICANT: KATO, MASATO  
; TITLE OF INVENTION: CONSTRUCTION AND USE OF SYNTHETIC CONSTRUCTS ENCODING SYNDECAN  
; FILE REFERENCE: 101353-232  
; CURRENT APPLICATION NUMBER: US/10/776,989  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: 09/723,677  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 08/471,970  
; PRIOR FILING DATE: 1995-06-06  
; PRIOR APPLICATION NUMBER: 08/078,683  
; PRIOR FILING DATE: 1993-06-17  
; PRIOR APPLICATION NUMBER: 07/856,869  
; PRIOR FILING DATE: 1992-03-24  
; PRIOR APPLICATION NUMBER: 07/757,654  
; PRIOR FILING DATE: 1991-09-06  
; PRIOR APPLICATION NUMBER: 07/746,797  
; PRIOR FILING DATE: 1991-08-12  
; PRIOR APPLICATION NUMBER: 07/331,585  
; PRIOR FILING DATE: 1989-03-29  
; NUMBER OF SEQ ID NOS: 46  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 175  
; TYPE: PRT  
; ORGANISM: MUS SP;HOMO SAPIEN  
US-10-776-989-34

Query Match 73.1%; Score 361; DB 17; Length 175;  
Best Local Similarity 77.7%; Pred. No. 5.1e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVVAATPTSLISWDAAPVTVYRYITYGETGNSPVQEFVPPWASITATIS 60

Db 82 VSDVPRDLEVVAATPTSLISWDAAPVTVYRYITYGETGNSPVQEFVPPWASITATIS 141  
QY 61 GLKPGVDYITVYAVTSDTKSDTYKYDDPISINVRT 94  
Db 142 GLKPGVDYITVYAVTGRGDSPPASSKPSISINVRT 175  
RESULT 15  
US-09-775-964-25  
; Sequence 25, Application US/09775964  
; Publication No. US20030087437A1  
; GENERAL INFORMATION:  
; APPLICANT: Asada, Kiyozo  
; Uemori, Takashi  
; Koyama, No. US20030087437A1  
; Hashino, Kimikazu  
; Kato, Ikunoshin  
; TITLE OF INVENTION: METHOD FOR GENE TRANSFER INTO TARGET  
; CELLS WITH RETROVIRUS  
; NUMBER OF SEQUENCES: 39  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: WEISER & ASSOCIATES  
; STREET: 230 South Fifteenth Street, Suite 500  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/775,964  
FILING DATE: 20-Feb-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/366,009  
FILING DATE: 02-Aug-1999  
APPLICATION NUMBER: 08/809,156  
FILING DATE: <Unknown>  
APPLICATION NUMBER: JP 294382/1995  
FILING DATE: 13-NOV-1995  
APPLICATION NUMBER: JP 051847/1996  
FILING DATE: 08-MAR-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Weiser, Gerard J.  
REGISTRATION NUMBER: 19,763  
REFERENCE/DOCKET NUMBER: 977.6507P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 215-875-8383  
TELEFAX: 215-875-8394  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 274 amino acids  
TYPE: amino acid  
STRANDEDNESS: <Unknown>  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-775-964-25

Query Match 73.1%; Score 361; DB 10; Length 274;  
Best Local Similarity 77.7%; Pred. No. 8.9e-33;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
QY 1 VSDVPRDLEVVAATPTSLISWDAAPVTVYRYITYGETGNSPVQEFVPPWASITATIS 60  
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QY 61 GLKPGVDYITVYAVTSDTKSDTYKYDDPISINVRT 94



Db 238 GLKPGVDYTIIVYAVTGRGDSPASSKPISINVRT 271

Search completed: May 18, 2005, 15:50:05  
Job time : 135 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2005, 15:31:59 ; Search time 40 Seconds  
(without alignments)  
226.109 Million cell updates/sec

Title: US-09-688-566-81  
Perfect score: 494  
Sequence: 1 VSDVPRDLEVAAPTSLRI.....VTDKSDTYKYDDPISINVRT 94

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:\*  
1: Piri:\*  
2: Piri2:\*  
3: Piri3:\*  
4: Piri4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	2386	1 FNHU	fibronectin precu
2	354	71.7	2265	1 FNBO	fibronectin - bovi
3	333	67.4	2477	2 S14428	fibronectin precu
4	311	63.0	273	2 A28512	fibronectin - chic
5	311	63.0	1020	2 A29355	fibronectin - chic
6	262	53.0	2481	2 A43908	fibronectin - Afri
7	125	25.3	4006	2 T09070	probable tenascin
8	124	25.1	4135	2 T42629	tenascin-X - bovin
9	121	24.5	1353	1 JH0675	restriclin precurs
10	121	24.5	1746	1 S19694	tenascin precursor
11	116	23.5	1356	2 A45445	janusin precursor,
12	111	22.5	3566	1 A40701	tenascin-X precurs
13	110.5	22.4	1898	2 S46216	leukocyte antigen-
14	110	22.3	2019	1 J01322	tenascin precursor
15	108	21.9	933	2 A1930	cytotactin - chick
16	108	21.9	1810	1 A32230	tenascin precursor
17	106.5	21.6	2944	2 A54849	collagen alpha 1(V
18	105	21.3	2201	2 A32160	tenascin-C - pig
19	102	20.6	417	2 S65944	tenascin-X - huan
20	100	20.2	1912	2 A56178	protein-tyrosine-p
21	98.5	19.9	647	2 A43902	tenascin - eastern
22	96	19.4	1290	2 A56493	leucocyte common a
23	96	19.4	3124	2 A40020	collagen alpha 1(X
24	94	19.0	843	2 A40970	undulin 1 - human
25	92	18.6	1691	1 D54689	protein-tyrosine-p
26	92	18.6	1894	2 C54689	protein-tyrosine-p
27	91.5	18.5	147	2 S00848	fibronectin, trans
28	90.5	18.3	440	2 I50213	protein-tyrosine-p
29	88.5	17.9	189	2 S71465	fibronectin - chic

30	88.5	17.9	575	2 A54861	tenascin - rat (fr
31	87.5	17.7	90	2 I46162	fibronectin ED-B -
32	87	17.6	1897	1 TDHULK	leukocyte antigen-
33	86	17.4	1711	1 A55148	protein-tyrosine-p
34	83	16.8	860	2 I48839	tenascin-X - mouse
35	82	16.6	89	2 I46161	fibronectin ED-A -
36	82	16.6	1241	2 T37190	nephrin - human
37	81.5	16.5	929	2 I51027	type XII collagen
38	81.5	16.5	1747	2 A45974	collagen alpha 1(X
39	81.5	16.5	1857	2 S31212	collagen alpha 1(X
40	81.5	16.5	1888	2 S78476	collagen alpha 1(X
41	80	16.2	1914	2 T42635	tenascin Y precurs
42	79	16.0	2029	1 TDFELK	protein-tyrosine-p
43	78	15.8	1337	1 I38670	protein-tyrosine-p
44	77.5	15.7	445	2 B40970	undulin 2 - human
45	77	15.6	725	2 A90255	hypothetical prote

ALIGNMENTS

RESULT 1

FNHU  
fibronectin precursor [validated] - human  
N:Alternate names: fibronectin splice form ED-A  
C:Species: Homo sapiens (man)  
C:Date: 27-Nov-1985 #sequence revision 31-Mar-1993 #text change 09-Jul-2004  
C:Accession: A26460; A26284; S03917; A24854; A24476; A91008; A93529; A21011; A90495; A22  
R:Dean, D.C.; Bowlin, C.L.; Bourgeois, S.  
Proc. Natl. Acad. Sci. U.S.A. 84, 1876-1880, 1987  
A:Title: Cloning and analysis of the promoter region of the human fibronectin gene.  
A:Reference number: A26460; MUID:87175578; PMID:3031656  
A:Accession: A26460  
A:Molecule type: DNA  
A:Residues: 1-49 <DEA>  
A:Cross-references: UNIPROT:P02751; UNIPROT:Q14327; GB:M15801; NID:G182686; PIDN:AAAS337  
R:Oldberg, A.; Ruoslahti, E.  
J. Biol. Chem. 261, 2113-2116, 1986  
A:Title: Evolution of the fibronectin gene.  
A:Reference number: A26284; MUID:86111901; PMID:3003095  
A:Accession: A26284  
A:Molecule type: DNA  
A:Residues: 1447-1540 <OLD>  
A:Cross-references: GB:M12549; NID:G182688  
R:Paolella, G.; Henchcliffe, C.; Sebastio, G.; Baralle, F.E.  
Nucleic Acids Res. 16, 3545-3557, 1988  
A:Title: Sequence analysis and in vivo expression show that alternative splicing of ED-B  
A:Reference number: S00848; MUID:88233940; PMID:3375063  
A:Accession: S03917  
A:Molecule type: DNA  
A:Residues: 1594-1767, 'V', 1769-1783 <PAO>  
A:Cross-references: EMBL:X07718; NID:G31402  
A:Note: the authors translated the codon AAC for residue 1631 as Asp  
R:Vibe-Pedersen, K.; Magnusson, S.; Baralle, F.E.  
FEBS Lett. 207, 287-291, 1986  
A:Title: Donor and acceptor splice signals within an exon of the human fibronectin gene:  
A:Reference number: A24854; MUID:87030929; PMID:3770201  
A:Accession: A24854  
A:Molecule type: DNA  
A:Residues: 1992-2147 <VIB>  
A:Cross-references: GB:X04530; NID:G31436  
R:Gutman, A.; Yamada, K.M.; Kornblihtt, A.  
FEBS Lett. 207, 145-148, 1986  
A:Title: Human fibronectin is synthesized as a pre-propolypeptide.  
A:Reference number: A24476; MUID:87030890; PMID:3770189  
A:Accession: A24476  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-14, 'Q', 16-38 <GUT>  
R:Kornblihtt, A.R.; Umezawa, K.; Vibe-Pedersen, K.; Baralle, F.E.  
EMBO J. 4, 1755-1759, 1985  
A:Title: Primary structure of human fibronectin: differential splicing may generate at l

A;Reference number: A91008; MUID:85284965; PMID:2992939  
 A;Accession: A91008  
 A;Status: nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 32-1344;1346-2080;2112-2386 <KOR>  
 A;Cross-references: GB:X02761  
 R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
 Nucleic Acids Res. 12, 5853-5868, 1984  
 A;Title: Human fibronectin: cell specific alternative mRNA splicing generates polypeptide  
 A;Reference number: A93529; MUID:84272258; PMID:6462919  
 A;Accession: A93529  
 A;Molecule type: mRNA  
 A;Residues: 973-2080;2112-2386 <K02>  
 A;Cross-references: GB:X00739  
 R;Oldberg, A.; Linney, E.; Ruoslahti, E.  
 J. Biol. Chem. 258, 10193-10196, 1983  
 A;Title: Molecular cloning and nucleotide sequence of a cDNA clone coding for the cell a  
 A;Reference number: A21011; MUID:83290929; PMID:6668418  
 A;Accession: A21011  
 A;Molecule type: mRNA  
 A;Residues: 1434-1537 <OL2>  
 A;Cross-references: GB:X00055; NID:gl82680; PIDN:AAA52459.1; PID:gl82683  
 R;Bernard, M.P.; Kolbe, M.; Weil, D.; Chu, M.L.  
 Biochemistry 24, 2698-2704, 1985  
 A;Title: Human cellular fibronectin: comparison of the carboxyl-terminal portion with ra  
 A;Reference number: A90495; MUID:85280409; PMID:2992573  
 A;Accession: A90495  
 A;Molecule type: mRNA  
 A;Residues: 1594-2386 <BER>  
 A;Cross-references: GB:M10905; NID:gl82696; PIDN:AAA52462.1; PID:gl82697  
 R;Umezawa, K.; Kornblitt, A.R.; Baralle, F.E.  
 FEBS Lett. 186, 31-34, 1985  
 A;Title: Isolation and characterization of cDNA clones for human liver fibronectin.  
 A;Reference number: A22245; MUID:85231203; PMID:2989004  
 A;Accession: A22245  
 A;Molecule type: mRNA  
 A;Residues: 1948-2067 <UME>  
 A;Cross-references: GB:M27589; NID:gl82705; PIDN:AAA52465.1; PID:gl82706  
 A;Accession: B22245  
 A;Molecule type: mRNA  
 A;Residues: 1975-1991;2017-2039 <UM2>  
 A;Cross-references: GB:M27590  
 R;Sekiguchi, K.; Kloe, A.M.; Kurachi, K.; Yoshitake, S.; Hakomori, S.  
 Biochemistry 25, 4936-4941, 1986  
 A;Title: Human liver fibronectin complementary DNAs: identification of two different mes  
 A;Reference number: I52394; MUID:87026578; PMID:3021206  
 A;Accession: I65273  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: mRNA  
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 A;Cross-references: GB:M14060; NID:gl82701; PIDN:AAA52464.1; PID:gl82704  
 R;Kornblitt, A.R.; Vibe-Pedersen, K.; Baralle, F.E.  
 Proc. Natl. Acad. Sci. U.S.A. 80, 3218-3222, 1983  
 A;Title: Isolation and characterization of cDNA clones for human and bovine fibronectins  
 A;Reference number: A21165; MUID:83221567; PMID:6304699  
 A;Accession: A21165  
 A;Molecule type: mRNA  
 A;Residues: 2291-2386 <K03>  
 A;Cross-references: GB:K00799; NID:gl82681; PIDN:AAA52460.1; PID:gl82684  
 R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
 J. Biol. Chem. 258, 12670-12674, 1983  
 A;Title: Primary structure of human plasma fibronectin.  
 A;Reference number: A92398; MUID:84032463; PMID:6630202  
 A;Accession: A92398  
 A;Molecule type: protein  
 A;Residues: 32-47, 'C', 49-51, 'S', 53-72, 'A', 74-290 <GAR1>  
 R;Garcia-Pardo, A.; Gold, L.I.  
 Arch. Biochem. Biophys. 304, 181-188, 1993  
 A;Title: Further characterization of the binding of fibronectin to gelatin reveals the fi  
 A;Reference number: S34791; MUID:93312001; PMID:8323285  
 A;Accession: S34791  
 A;Molecule type: protein  
 A;Residues: 291-300;551-560 <GAR2>

R;Griffin, C.A.; Calaycay, J.; Shively, J.E.; Smith, R.L.  
 Thromb. Res. 43, 469-477, 1986  
 A;Title: Two plasma fibronectin fragments with different gelatin-binding properties.  
 A;Reference number: A60904; MUID:87019725; PMID:3532418  
 A;Accession: A60904  
 A;Molecule type: protein  
 A;Residues: 293-301 <GRI>  
 R;Calaycay, J.; Pande, H.; Lee, T.; Borsi, L.; Siri, A.; Shively, J.E.; Zardi, L.  
 J. Biol. Chem. 260, 12136-12141, 1985  
 A;Title: Primary structure of a DNA- and heparin-binding domain (domain III) in human p  
 A;Reference number: A23901; MUID:86008277; PMID:3900070  
 A;Accession: A23901  
 A;Molecule type: protein  
 A;Residues: 616-677, 'O', 679-703, 'PT' <CAL>  
 R;Pierschbacher, M.D.; Ruoslahti, E.; Sundelin, J.; Lind, P.; Peterson, P.A.  
 J. Biol. Chem. 257, 9593-9597, 1982  
 A;Title: The cell attachment domain of fibronectin. Determination of the primary struct  
 A;Reference number: A92386; MUID:82265604; PMID:7050098  
 A;Accession: A92386  
 A;Molecule type: protein  
 A;Residues: 1441-1548 <PIB>  
 A;Note: residues 1524-1527 are responsible for the cell-binding activity  
 R;Garcia-Pardo, A.; Rostagno, A.; Frangione, B.  
 Biochem. J. 241, 923-928, 1987  
 A;Title: Primary structure of human plasma fibronectin. Characterization of a 38 kDa do  
 A;Reference number: A32517; MUID:87241275; PMID:3593230  
 A;Accession: A32517  
 A;Molecule type: protein  
 A;Residues: 1589-1630, 'T', 1722-2058 <GAR3>  
 R;Tresselt, T.; McCarthy, J.B.; Calaycay, J.; Lee, T.D.; Legesse, K.; Shively, J.E.; Pan  
 Biochem. J. 274, 731-738, 1991  
 A;Title: Human plasma fibronectin. Demonstration of structural differences between the i  
 A;Reference number: S14357; MUID:91190085; PMID:2012601  
 A;Accession: S14357  
 A;Molecule type: protein  
 A;Residues: 1614-1630, 'T', 1722-2081, 2113-2244 <TRE>  
 R;Garcia-Pardo, A.; Pearlstein, E.; Frangione, B.  
 J. Biol. Chem. 260, 10320-10325, 1985  
 A;Title: Primary structure of human plasma fibronectin. Characterization of a 31,000-da  
 A;Reference number: A23891; MUID:85261459; PMID:4019516  
 A;Accession: A23891  
 A;Molecule type: protein  
 A;Residues: 2071-2080;2112-2356 <GAR4>  
 C;Comment: The extra domain and connecting strand 3 are subject to developmental and ti  
 C;Comment: The cellular and plasma fibronectins are high molecular weight glycoproteins,  
 ation, and transformation.  
 C;Genetics:  
 A;Gene: GDB:FN1  
 A;Cross-references: GDB:119135; OMIM:135600  
 A;Map position: 2Q34-2Q34  
 A;Introns: 49/3; 1266/1; 1357/1; 1447/1; 1487/1; 1541/1; 1631/1; 1721/1; 1991/1; 2145/1  
 C;Superfamily: fibronectin; fibronectin type I repeat homology <1F2>  
 C;Keywords: acute phase; alternative splicing; cell adhesion; collagen binding; duplica  
 F;1-26/Domain: signal sequence #status predicted <SIG>  
 F;27-31/Domain: propeptide #status predicted <PRO>  
 F;32-2386/Product: fibronectin #status experimental <MAT>  
 F;52-272/Domain: fibrin and heparin binding <FHB>  
 F;52-87/Domain: fibronectin type I repeat homology <1F1>  
 F;97-135/Domain: fibronectin type I repeat homology <1F2>  
 F;141-179/Domain: fibronectin type I repeat homology <1F3>  
 F;186-225/Domain: fibronectin type I repeat homology <1F4>  
 F;231-270/Domain: fibronectin type I repeat homology <1F5>  
 F;308-608/Domain: collagen binding <CBR>  
 F;308-342/Domain: fibronectin type I repeat homology <1F6>  
 F;360-401/Domain: fibronectin type II repeat homology <2F1>  
 F;420-461/Domain: fibronectin type II repeat homology <2F2>  
 F;470-508/Domain: fibronectin type I repeat homology <1F8>  
 F;518-555/Domain: fibronectin type I repeat homology <1F8>  
 F;561-599/Domain: fibronectin type I repeat homology <1F9>  
 F;609-692/Domain: fibronectin type III repeat homology <3FA>  
 F;616-706/Domain: heparin binding <HPB>  
 F;719-801/Domain: fibronectin type III repeat homology <3FB>  
 F;810-891/Domain: fibronectin type III repeat homology <3FC>

F;1055-1134/Domain: fibronectin type III repeat homology <FN3F>  
F;1142-1227/Domain: fibronectin type III repeat homology <FN3G>  
F;1235-1318/Domain: fibronectin type III repeat homology <FN3H>  
F;1326-1404/Domain: fibronectin type III repeat homology <GN3I>  
F;1410-1517/Domain: cell attachment <CAD>  
F;1416-1502/Domain: fibronectin type III repeat homology <FN3J>  
F;1493-1495/Region: cell attachment (R-G-D) motif  
F;1510-1592/Domain: fibronectin type III repeat homology <FN3K>  
F;1600-1870/Domain: heparin binding <HB2>  
F;1600-1682/Domain: fibronectin type III repeat homology <FN3L>  
F;1692-1773/Domain: fibronectin type III repeat homology <FN3M>  
F;1781-1863/Domain: fibronectin type III repeat homology <FN3N>  
F;1970-1972/Region: cell attachment (R-G-D) motif  
F;1982-2062/Domain: fibronectin type III repeat homology <FN3O>  
F;1985-2216/Domain: fibrin binding <FB2>  
F;2085-2124/Domain: fibronectin type I repeat homology <F10>  
F;2130-2167/Domain: fibronectin type I repeat homology <F11>  
F;2174-2209/Domain: fibronectin type I repeat homology <F12>  
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental  
F;3/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of fibrin) #status experimente  
F;21-47,45-56,66-94,92-104,110-138,136-148,155-184,182-194,200-229,227-239,277-304,302-3  
7,2155-2167,2174-2200,2198-2209/Disulfide bonds: #status predicted  
F;399,497,511,846,976,1213,1987/Binding site: carbohydrate (Asn) (covalent) #status expe  
F;1205,1692/Binding site: carbohydrate (Asn) (covalent) #status absent  
F;1943,1944/Binding site: carbohydrate (Thr) (covalent) #status experimental  
F;2246/Disulfide bonds: interchain (to 2250) #status predicted  
F;2250/Disulfide bonds: interchain (to 2246) #status predicted  
F;2263/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 71.7%; Score 354; DB 1; Length 2265;  
Best Local Similarity 74.5%; Pred. No. 6.4e-28;  
Matches 70; Conservative 7; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDPRDLVVAAPTSRLSIWNRSGLQSRYYRITYTGETGNSPVOEFTVPWPWASIIATIS 60  
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Db 1416 VSDPRDLVVAAPTSRLSIWNRSGLQSRYYRITYTGETGNSPVOEFTVPWGSKSTATIS 1475  
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Qy 61 GLKPGVDYTIITVYATGKSDTYKYDDPISINRYT 94  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1476 GLKPGVDYTIITVYATGKSDPASPSPKPSINRYT 1509  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3  
S14428  
fibronectin precursor - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
C:Accession: S14428; S12455; A22319; S46203; S00459; A27252; 159049  
R:Hynes, R.O.  
submitted to the EMBL Data Library, July 1989  
A:Reference number: S14428  
A:Accession: S14428  
A:Molecule type: mRNA  
A:Residues: 1-2477 <HYN>  
A:Cross-references: UNIPROT:P04937; EMBL:X15906; NID:g56163; PIDN:CAA34020.1; PID:g56164  
R:Schwarzbauer, J.E.; Patel, R.S.; Fonda, D.; Hynes, R.O.  
EMBO J. 6, 2573-2580, 1987  
A:Title: Multiple sites of alternative splicing of the rat fibronectin gene transcript.  
A:Reference number: S12455; MUID:88054951; PMID:2445560  
A:Accession: S12455  
A:Molecule type: mRNA  
A:Residues: 609-1810, 'T', 1812-2283 <SCH>  
A:Cross-references: EMBL:X15906  
R:Ramkun, J.W.; Schwarzbauer, J.E.; Hynes, R.O.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5140-5144, 1984  
A:Title: A single rat fibronectin gene generates three different mRNAs by alternative sp  
A:Reference number: A22319; MUID:84298097; PMID:6089177  
A:Accession: A22319  
A:Molecule type: DNA  
A:Residues: 2052-2237 <TAM>  
R:Ralkenberg, C.; Enghild, J.J.; Thogersen, I.B.; Salvesen, G.; Akerstrom, B.  
Biochem. J. 301, 745-751, 1994

A>Title: Isolation and characterization of fibronectin-alpha(1)-microglobulin complex in  
A/Reference number: S46203; MUID:94330948; PMID:7519849  
A/Accession: S46203  
A>Status: preliminary  
A/Molecule type: protein  
A/Residues: 1183-1192; 'GLN', 1268, 'P', 1270-1271, 'D', 1273, 'CF', 1276, 'PY', 1385-1399 <FAL>  
R./Patel, R.S.; Odermatt, E.; Schwarzbauer, J.E.; Hynes, R.O.  
EMBO J. 6, 2565-2572, 1987  
A>Title: Organization of the fibronectin gene provides evidence for exon shuffling during  
A/Reference number: S00459; MUID:88054950; PMID:3119323  
A/Accession: S00459  
A/Molecule type: DNA  
A/Residues: 1-139; 2382-2477 <PAT>  
A/Accession: EMBL:X05831  
A/Note: the authors translated the codon CCG for residues 51 and 94 as Ala  
R./Schwarzbauer, J.E.; Tamkun, J.W.; Lemischka, I.R.; Hynes, R.O.  
Cell 55, 421-431, 1983  
A>Title: Three different fibronectin mRNAs arise by alternative splicing within the coding  
A/Reference number: A27252; MUID:84082067; PMID:6317187  
A/Accession: A27252  
A/Molecule type: mRNA  
A/Residues: 1586-1720, 'T', 1722, 1813-2477 <SC2>  
R./Odermatt, E.; Tamkun, J.W.; Hynes, R.O.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6571-6575, 1985  
A>Title: Repeating modular structure of the fibronectin gene: Relationship to protein structure  
A/Reference number: I59049; MUID:86016741; PMID:3863113  
A/Accession: I59049  
A>Status: translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1722-1810 <RES>  
A/Cross-references: GB:M11750; NID:G204164; PIDN:AAA41170.1; PID:G554437  
C/Genetics:  
A/Introns: 51/1; 94/1; 2416/3; 2454/3  
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat  
C/Keywords: alternative splicing; cell adhesion; collagen binding; disulfide bond; duplication  
F/1-32/Domain: signal sequence #status predicted <SIG>  
F/33-2477/Product: fibronectin #status predicted <MAT>  
F/53-88/Domain: fibronectin type I repeat homology <1F1>  
F/98-136/Domain: fibronectin type I repeat homology <1F2>  
F/142-180/Domain: fibronectin type I repeat homology <1F3>  
F/187-226/Domain: fibronectin type I repeat homology <1F4>  
F/232-271/Domain: fibronectin type I repeat homology <1F5>  
F/308-342/Domain: fibronectin type I repeat homology <1F6>  
F/360-401/Domain: fibronectin type II repeat homology <2F1>  
F/420-461/Domain: fibronectin type II repeat homology <2F2>  
F/470-508/Domain: fibronectin type I repeat homology <1F7>  
F/518-555/Domain: fibronectin type I repeat homology <1F8>  
F/561-599/Domain: fibronectin type I repeat homology <1F9>  
F/609-692/Domain: fibronectin type III repeat homology <FN3A>  
F/718-800/Domain: fibronectin type III repeat homology <FN3B>  
F/809-890/Domain: fibronectin type III repeat homology <FN3C>  
F/905-987/Domain: fibronectin type III repeat homology <FN3D>  
F/995-1076/Domain: fibronectin type III repeat homology <FN3E>  
F/1085-1164/Domain: fibronectin type III repeat homology <FN3F>  
F/1172-1257/Domain: fibronectin type III repeat homology <FN3G>  
F/1265-1348/Domain: fibronectin type III repeat homology <FN3H>  
F/1356-1439/Domain: fibronectin type III repeat homology <FN3I>  
F/1447-1529/Domain: fibronectin type III repeat homology <FN3J>  
F/1537-1619/Domain: fibronectin type III repeat homology <FN3K>  
F/1614-1616/Region: cell attachment (R-G-D) motif  
F/1631-1713/Domain: fibronectin type III repeat homology <FN3L>  
F/1721-1803/Domain: fibronectin type III repeat homology <FN3M>  
F/1811-1893/Domain: fibronectin type III repeat homology <FN3N>  
F/1903-1984/Domain: fibronectin type III repeat homology <FN3O>  
F/1992-2074/Domain: fibronectin type III repeat homology <FN3P>  
F/2181-2183/Region: cell attachment (R-G-D) motif  
F/2193-2273/Domain: fibronectin type III repeat homology <FN3Q>  
F/2296-2335/Domain: fibronectin type I repeat homology <1F10>  
F/2341-2378/Domain: fibronectin type I repeat homology <1F11>  
F/2385-2420/Domain: fibronectin type I repeat homology <1F12>  
F/3385-3420/Domain: fibronectin type I repeat homology <1F13>  
F/353-79, 77-88, 98-126, 124-136, 142-170, 168-180, 187-216, 214-226, 232-261, 259-271, 308-335, 333-368, 2366-2378, 2385-2411, 2409-2420/Disulfide bonds: #status predicted  
F/2458/Disulfide bonds: interchain (to 2462) #status predicted

F/2462/Disulfide bonds: interchain (to 2458) #status predicted  
Query Match 67.4%; Score 333; DB 2; Length 2477;  
Best Local Similarity 68.1%; Pred. No. 1e-25; Mismatches 20; Indels 0; Gaps 0;  
Matches 64; Conservative 10;  
QY 1 VSDVPRDLEVAATPSTLSLISWNSRGLQSRYYRITYGTGNSPVQEFVPPWASIIATIS 60  
Db 1537 VSDVPRDLEVIATPSTLSLISWNSRGLQSRYYRITYGTGNSPVQEFVPPWASIIATIS 1596  
QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
Db 1597 NIKPGADYTIIVYAVTGRGDSPASSKPVSIYQT 1630  
RESULT 4  
A28512  
Fibronectin - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
R./Kubomura, S.; Ohara, M.; Karasaki, Y.; Taniguchi, H.; Gotoh, S.; Tsuda, T.; Higashi, T.  
Biochim. Biophys. Acta 910, 171-181, 1987  
A/Title: Genetic analysis of the cell binding domain region of the chicken fibronectin  
A/Reference number: A28512; MUID:88050950; PMID:2823899  
A/Accession: A28512  
A/Molecule type: DNA  
A/Residues: 1-273 <KUB>  
A/Cross-references: UNIPROT:P11722; GB:X06533; NID:963393; PIDN:CAA29781.1; PID:G295716  
A/Note: the authors translated the codon CCG for residue 190 as Gln, CAG for residue 243  
C/Genetics:  
A/Introns: 90/1; 129/1; 184/1; 236/1  
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat  
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter  
F/1-82/Domain: fibronectin type III repeat homology (fragment) <FN3I>  
F/90-172/Domain: fibronectin type III repeat homology <FN3J>  
F/167-169/Region: cell attachment (R-G-D) motif  
F/184-266/Domain: fibronectin type III repeat homology <FN3K>  
Query Match 63.0%; Score 311; DB 2; Length 273;  
Best Local Similarity 64.9%; Pred. No. 1.5e-24; Mismatches 22; Indels 0; Gaps 0;  
Matches 61; Conservative 11;  
QY 1 VSDVPRDLEVAATPSTLSLISWNSRGLQSRYYRITYGTGNSPVQEFVPPWASIIATIS 60  
Db 90 VSDVPRDLEVNPTSTLSLISWNSRGLQSRYYRITYGTGNSPVQEFVPPWASIIATIS 149  
QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94  
Db 150 GLKPGVDYTIIVYAVTGRGDSPASSKPVTVTYKT 183  
RESULT 5  
A29355  
Fibronectin - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004  
C/Accession: A29355  
R./Norton, P.A.; Hynes, R.O.  
Mol. Cell. Biol. 7, 4297-4307, 1987  
A/Title: Alternative splicing of chicken fibronectin in embryos and in normal and transfe  
A/Reference number: A29355; MUID:88142820; PMID:2830487  
A/Accession: A29355  
A/Molecule type: mRNA  
A/Residues: 1-1020 <NOR>  
A/Cross-references: UNIPROT:P11722  
C/Genetics:  
A/Introns: 176/3  
C/Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat  
C/Keywords: alternative splicing; duplication; extracellular matrix; glycoprotein; heter  
F/1-86/Domain: fibronectin type III repeat homology <FN3H>  
F/92-177/Domain: fibronectin type III repeat homology <FN3I>  
F/180-262/Domain: fibronectin type III repeat homology <FN3J>

A;Residues: 1-2491 <D>S>

A;Cross-references: GB:M7820

A;Note: sequence extracted from NCBI backbone (NCBIP:77473)

C;Superfamily: fibronectin; fibronectin type I repeat homology; fibronectin type II repeat homology; fibronectin type III repeat homology; glycoprotein; heterodimer

C;Keywords: duplication; extracellular matrix; glycoprotein; heterodimer

F;55-90/Domain: fibronectin type I repeat homology <F1>

F;100-138/Domain: fibronectin type I repeat homology <F2>

F;144-182/Domain: fibronectin type I repeat homology <F3>

F;189-228/Domain: fibronectin type I repeat homology <F4>

F;234-273/Domain: fibronectin type I repeat homology <F5>

F;309-343/Domain: fibronectin type I repeat homology <F6>

F;361-402/Domain: fibronectin type II repeat homology <F1>

F;421-462/Domain: fibronectin type II repeat homology <F2>

F;471-509/Domain: fibronectin type I repeat homology <F7>

F;519-556/Domain: fibronectin type I repeat homology <F8>

F;562-600/Domain: fibronectin type I repeat homology <F9>

F;610-693/Domain: fibronectin type III repeat homology <FN3A>

F;719-801/Domain: fibronectin type III repeat homology <FN3B>

F;810-891/Domain: fibronectin type III repeat homology <FN3C>

F;906-988/Domain: fibronectin type III repeat homology <FN3D>

F;996-1077/Domain: fibronectin type III repeat homology <FN3E>

F;1086-1165/Domain: fibronectin type III repeat homology <FN3F>

F;1173-1258/Domain: fibronectin type III repeat homology <FN3G>

F;1266-1349/Domain: fibronectin type III repeat homology <FN3H>

F;1357-1440/Domain: fibronectin type III repeat homology <FN3I>

F;1448-1530/Domain: fibronectin type III repeat homology <FN3J>

F;1538-1620/Domain: fibronectin type III repeat homology <FN3K>

F;1615-1617/Region: cell attachment (R-G-D) motif

F;1632-1714/Domain: fibronectin type III repeat homology <FN3L>

F;1722-1804/Domain: fibronectin type III repeat homology <FN3M>

F;1812-1894/Domain: fibronectin type III repeat homology <FN3N>

F;1904-1985/Domain: fibronectin type III repeat homology <FN3O>

F;1993-2075/Domain: fibronectin type III repeat homology <FN3P>

F;2197-2277/Domain: fibronectin type III repeat homology <FN3Q>

F;2301-2340/Domain: fibronectin type I repeat homology <F10>

F;2346-2383/Domain: fibronectin type I repeat homology <F11>

F;2390-2425/Domain: fibronectin type I repeat homology <F12>





A:Molecule type: mRNA  
A:Residues: 1-1356 <FUS2>  
A:Cross-references: EMBL:Z18630; NID:G57961; PIDN:CAA79229.1; PID:G57962  
C:Superfamily: restrictin; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
C:Keywords: alternative splicing; duplication; fibronectin type III repeat homology; glycoprotein; oligo  
F:1-1356/Product: janusin, long form #status experimental <MAT>  
F:1-172,863-1356/Product: janusin, short form #status experimental <ALT>  
F:204-230/Domain: EGF homology <EG1>  
F:235-261/Domain: EGF homology <EG2>  
F:266-292/Domain: EGF homology <EG3>  
F:297-323/Domain: EGF homology <EG4>  
F:325-405/Domain: fibronectin type III repeat homology <FN1>  
F:413-494/Domain: fibronectin type III repeat homology <FN2>  
F:502-584/Domain: fibronectin type III repeat homology <FN3>  
F:592-676/Domain: fibronectin type III repeat homology <FN4>  
F:684-764/Domain: fibronectin type III repeat homology <FN5>  
F:772-854/Domain: fibronectin type III repeat homology <FN6>  
F:1038-1118/Domain: fibronectin type III repeat homology <FN7>  
F:1133-1341/Domain: fibrinogen beta/gamma homology <FBG>  
Query Match 23.5%; Score 116; DB 2; Length 1356;  
Best Local Similarity 27.4%; Pred. No. 0.0011;  
Matches 34; Conservative 18; Mismatches 36; Indels 36; Gaps 3;  
Qy 3 DVPRDLVVAATPTSLRSLGQSRVYRITVGTGNSPVQSFVTPPWSIATISGL 62  
Db 686 DSPRLDMVTASSETSLIWTKASGPDHYRITETPPSGIS--SEVTVPDRDTSYTLTDL 743  
Qy 63 KPGVDYITITVA-----VTDKSDTYKYDDP-----I 88  
Db 744 EPGAIIISITAEGRQOSLESTVDATFGFRPISHLHFHSHTSSVNIWSDSPPADRL 803  
Qy 89 SINY 92  
Db 804 ILNY 807  
RESULT 12  
A40701  
tenascin-X precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A40701; A33725; C42175  
R:Bristow, J.; Tee, M.K.; Gitelman, S.E.; Mellon, S.H.; Miller, W.L.  
J. Cell Biol. 122, 265-278, 1993  
A:Title: Tenascin-X: a novel extracellular matrix protein encoded by the human XB gene c  
A:Reference number: A40701; MUID:93300909; PMID:7686164  
A:Accession: A40701  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-3566 <BRI>  
A:Cross-references: UNIPROT:P22105; UNIPROT:Q9UC11; EMBL:X71937  
R:Morel, Y.; Bristow, J.; Gitelman, S.E.; Miller, W.L.  
Proc. Natl. Acad. Sci. U.S.A. 86, 6582-6586, 1989  
A:Title: Transcript encoded on the opposite strand of the human steroid 21-hydroxylase/c  
A:Reference number: A33725; MUID:89367293; PMID:2475872  
A:Accession: A33725  
A:Molecule type: mRNA  
A:Residues: 2748-3199, 'V', 3201-3298, 'E', 3299-3314, 'G', 3316-3566 <MOR>  
A:Cross-references: GB:M25813; NID:g183069; PIDN:AAA35884.1; PID:g183070  
R:Matsumoto, K.; Arai, M.; Ishihara, N.; Ando, A.; Inoko, H.; Ikemura, T.  
Genomics 12, 485-491, 1992  
A:Title: Cluster of fibronectin type III repeats found in the human major histocompatibi  
enacin.  
A:Reference number: A42175; MUID:92217969; PMID:1373119  
A:Accession: C42175  
A:Molecule type: DNA  
A:Residues: 1849-1936 <MAT>  
A:Experimental source: clone 3.9kF3-1  
A:Note: sequence extracted from NCI backbone (NCBIP:95694)  
C:Genetics:  
A:Gene: GDB:TNXA; D6S103E; TNX; XA; XB  
A:Cross-references: GDB:568487; OMIM:600261

A:Map position: 6p21.3-6p21.3  
C:Superfamily: tenascin-X; EGF homology; fibrinogen beta/gamma homology; fibronectin typ  
C:Keywords: extracellular matrix; glycoprotein  
F:435-461/Domain: EGF homology <EGF>  
F:748-828/Domain: fibronectin type III repeat homology <3F1>  
F:829-856/Domain: fibronectin type III repeat homology #status atypical <3F2>  
F:873-953/Domain: fibronectin type III repeat homology <3F3>  
F:975-1055/Domain: fibronectin type III repeat homology <3F4>  
F:1078-1158/Domain: fibronectin type III repeat homology <3F5>  
F:1167-1247/Domain: fibronectin type III repeat homology <3F6>  
F:1248-1317/Domain: fibronectin type III repeat homology #status atypical <3F7>  
F:1323-1403/Domain: fibronectin type III repeat homology <3F8>  
F:1412-1492/Domain: fibronectin type III repeat homology <3F9>  
F:1510-1590/Domain: fibronectin type III repeat homology #status atypical <3F10>  
F:1618-1676/Domain: fibronectin type III repeat homology <3F11>  
F:1678-1749/Domain: fibronectin type III repeat homology #status atypical <3F12>  
F:1751-1831/Domain: fibronectin type III repeat homology <3F13>  
F:1849-1929/Domain: fibronectin type III repeat homology <3F14>  
F:1955-2035/Domain: fibronectin type III repeat homology <3F15>  
F:2061-2141/Domain: fibronectin type III repeat homology <3F16>  
F:2167-2246/Domain: fibronectin type III repeat homology <3F17>  
F:2274-2354/Domain: fibronectin type III repeat homology <3F18>  
F:2382-2462/Domain: fibronectin type III repeat homology <3F19>  
F:2488-2568/Domain: fibronectin type III repeat homology <3F20>  
F:2584-2664/Domain: fibronectin type III repeat homology <3F21>  
F:2677-2757/Domain: fibronectin type III repeat homology <3F22>  
F:2771-2851/Domain: fibronectin type III repeat homology <3F23>  
F:2878-2958/Domain: fibronectin type III repeat homology <3F24>  
F:2977-3067/Domain: fibronectin type III repeat homology #status atypical <3F25>  
F:3078-3159/Domain: fibronectin type III repeat homology <3F26>  
F:3167-3247/Domain: fibronectin type III repeat homology <3F27>  
F:3255-3334/Domain: fibronectin type III repeat homology <3F28>  
F:3349-3557/Domain: fibrinogen beta/gamma homology <FBG>  
Query Match 22.5%; Score 111; DB 1; Length 3566;  
Best Local Similarity 31.9%; Pred. No. 0.011;  
Matches 30; Conservative 18; Mismatches 40; Indels 6; Gaps 3;  
Qy 1 VSDVPRDLVVAATPTSLRSLGQSRVYRITVGTGNSPVQSFVTPPWSIATIS 60  
Db 748 VIDGPDRLRVSVTPTTLEGLRPPQAEVDFVSVY-VSADNQVR-LEVPPETDGTLLT 805  
Qy 61 GLKPGVDYITITVAVTDKSDTYKYDDPISINYRT 94  
Db 806 DLMPGVEYVTVTAERGRAVSVY---PASVRANT 835  
RESULT 13  
S46216  
leukocyte antigen-related protein precursor - rat  
N:Alternate names: leukocyte common antigen homology  
N:Contains: protein-tyrosine-phosphatase (EC 3.1.3.48)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 20-Feb-1995 #sequence revision 20-Feb-1995 #text\_change 09-Jul-2004  
C:Accession: S46216; S23252; A41032; A33154  
R:Zhang, W.R.; Hashimoto, N.; Ahmad, F.; Ding, W.; Goldstein, B.J.  
Biochem. J. 302, 39-47, 1994  
A:Title: Molecular cloning and expression of a unique receptor-like protein-tyrosine-pho  
A:Reference number: S46216; MUID:94347119; PMID:8068021  
A:Accession: S46216  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-1898 <ZHA>  
A:Cross-references: UNIPROT:Q64604; EMBL:L11586; NID:G205132; PIDN:AAC37655.1; PID:G2051  
R:Hashimoto, N.; Zhang, W.R.; Goldstein, B.J.  
Biochem. J. 284, 569-576, 1992  
A:Title: Insulin receptor and epidermal growth factor receptor dephosphorylation by thre  
A:Reference number: S23126; MUID:92287069; PMID:1599438  
A:Accession: S23126  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1361-1604; 1649-1898 <HAS>  
R:Pot, D.A.; Woodford, T.A.; Ramboutsika, E.; Haun, R.S.; Dixon, J.E.

J. Biol. Chem. 266, 19688-19696, 1991  
A:Title: Cloning, bacterial expression, purification, and characterization of the cytoplasmic domain of the mouse tenascin protein.  
A:Reference number: A41032; MUID:92011772; PMID:1918076  
A:Accession: A41032  
A:Molecule type: mRNA  
A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <POT>  
A:Cross-references: GB:M60103; NID:G205130; PID:AAA41510.1; PID:G205131  
R:Pot, D.A.; Woodford, T.A.; Remboutsika, E.; Haun, R.S.; Dixon, J.E.  
submitted to the Protein Sequence Database, December 1990  
A:Reference number: A33154  
A:Accession: A33154  
A:Molecule type: mRNA  
A:Residues: 1035-1072, 'S', 1074-1433, 'T', 1435-1638, 'N', 1640-1642, 'HT', 1645-1898 <PO2>  
C:Comment: Only the first of the two domains homologous with protein-tyrosine-phosphatase.  
C:Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology; oxy  
C:Keywords: duplication; glycoprotein; phosphoprotein; phosphoric monoester hydrolase; tyrosine phosphorylation  
F:1-27/Domain: (or 1-26) signal sequence #status predicted <SIG>  
F:28-1898/Product: (or 27-1898) leukocyte antigen-related protein #status predicted <MAT>  
F:28-1251/Domain: (or 27-1251) extracellular #status predicted <EXT>  
F:47-109/Domain: immunoglobulin homology <IMM1>  
F:149-209/Domain: immunoglobulin homology <IMM2>  
F:246-300/Domain: immunoglobulin homology <IMM3>  
F:318-400/Domain: fibronectin type III repeat homology <FN3A>  
F:413-499/Domain: fibronectin type III repeat homology <FN3B>  
F:511-593/Domain: fibronectin type III repeat homology <FN3C>  
F:606-695/Domain: fibronectin type III repeat homology <FN3D>  
F:708-799/Domain: fibronectin type III repeat homology <FN3E>  
F:811-895/Domain: fibronectin type III repeat homology <FN3F>  
F:906-990/Domain: fibronectin type III repeat homology <FN3G>  
F:1002-1079/Domain: fibronectin type III repeat homology <FN3H>  
F:1252-1275/Domain: (or 1259-1275) transmembrane #status predicted <TM>  
F:1276-1898/Domain: intracellular #status predicted <INT>  
F:1286-1898/Domain: leukocyte common antigen cytosolic domain homology <LAC>  
F:1366-1897/Domain: protein-tyrosine-phosphatase homology <PTP1>  
F:1655-1878/Domain: protein-tyrosine-phosphatase homology <PTP2>  
F:54-107,156-207,253-298/disulfide bonds: #status predicted  
F:117,250,295,721,957/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:1539/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1545/Binding site: substrate phosphate (Arg) #status predicted  
F:1830/Active site: Cys (phosphocysteine intermediate) #status predicted  
F:1836/Binding site: substrate phosphate (Arg) #status predicted  
Query Match 22.4%; Score 110.5; DB 2; Length 1898;  
Best Local Similarity 37.1%; Pred. No. 0.006;  
Matches 33; Conservative 10; Mismatches 35; Indels 11; Gaps 3;  
QY 2 SDVPRDLEVVAAFTSRLISW-----NRSGLSQRYRITY-----GETGNSFPVQFTVP 51  
DB 709 SGPPRKEVEPLNSTAVHSWKLVPENKQHGQIRGQVTVYVRLNGEPRGQPIIQDVMLA 768  
QY 52 PWASIAITISGLKGVVDYITVYAVTQKSD 80  
DB 769 E-AQETTSISGLTPEPTYSITVAAAYTKGD 796  
RESULT 14  
JQ1322  
tenascin precursor - mouse  
N:Alternate names: contactin; hexabrachion  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: JQ1322; A37936; B37936; S14571; S50209  
Gene 104, 177-185, 1991  
R:Saga, Y.; Teukamoto, T.; Jing, N.; Kusakabe, M.; Sakakura, T.  
A:Title: Murine tenascin: cDNA cloning, structure and temporal expression of isoforms.  
A:Reference number: JQ1322; MUID:92009211; PMID:1717349  
A:Accession: JQ1322  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-2019 <SAG>  
A:Cross-references: UNIPROT:Q64706; GB:D90343; NID:G220609; PID:BAAL4355.1; PID:G220610  
A:Experimental source: cell line 2H6GR

A:Note: the authors translated the codon ATG for residue 60 as Trp  
R:Weller, A.; Beck, S.; Ekblom, P.  
J. Cell Biol. 112, 355-362, 1991  
A:Title: Amino acid sequence of mouse tenascin and differential expression of two tenascin isoforms.  
A:Reference number: A37936; MUID:91107734; PMID:1703162  
A:Accession: A37936  
A:Status: Preliminary  
A:Molecule type: mRNA  
A:Residues: 1-201, 'E', 203-317, 'S', 319-620, 622-1010, 'N', 1012-1018, 'S', 1020-1024, 'H', 1026.  
A:Cross-references: GB:X56304  
A:Accession: B37936  
A:Molecule type: mRNA  
A:Status: preliminary; nucleic acid sequence not shown  
A:Residues: 1-201, 'E', 203-317, 'S', 319-620, 622-1010, 'N', 1012-1018, 'S', 1020-1024, 'H', 1026.  
A:Cross-references: GB:X56304  
R:Weller, A.; Beck, S.; Ekblom, P.  
submitted to the EMBL Data Library, August 1990  
A:Description: Amino acid sequence of mouse tenascin and differential expression of two isoforms.  
A:Reference number: S14571  
A:Accession: S14571  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-201, 'E', 203-317, 'S', 319-1018, 'S', 1020-1024, 'H', 1026-1305, 'S', 1307-2019 <W>  
A:Cross-references: EMBL:X56304; NID:G54768; PID:CAA39751.1; PID:G54769  
R:Glumoff, V.; Savontaus, M.; Vehanen, J.; Vuorio, E.  
Biochim. Biophys. Acta 1219, 613-622, 1994  
A:Title: Analysis of aggrecan and tenascin gene expression in mouse skeletal tissues by Northern blotting.  
A:Reference number: S50206; MUID:95035091; PMID:7524681  
A:Accession: S50209  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: mRNA  
A:Residues: 46-146 <GLU>  
A:Cross-references: EMBL:X80281  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994  
C:Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type III repeat homology  
C:Keywords: alternative splicing; calcium binding; cell adhesion; duplication; extracellular matrix  
F:1-22/Domain: signal sequence #status predicted <SIG>  
F:23-1071/Product: tenascin, long splice form #status predicted <MAT>  
F:23-1071,1527-2019/Product: tenascin, short splice form #status predicted <MAT2>  
F:408-434/Domain: EGF homology <EGF>  
F:622-703/Domain: fibronectin type III repeat homology <FN3A>  
F:711-793/Domain: fibronectin type III repeat homology <FN3B>  
F:802-884/Domain: fibronectin type III repeat homology <FN3C>  
F:892-976/Domain: fibronectin type III repeat homology <FN3D>  
F:984-1064/Domain: fibronectin type III repeat homology <FN3E>  
F:1073-1155/Domain: fibronectin type III repeat homology <FN3F>  
F:1346-1428/Domain: fibronectin type III repeat homology <FN3G>  
F:1437-1519/Domain: fibronectin type III repeat homology <FN3H>  
F:1527-1608/Domain: fibronectin type III repeat homology <FN3I>  
F:1616-1696/Domain: fibronectin type III repeat homology <FN3J>  
F:1704-1784/Domain: fibronectin type III repeat homology <FN3K>  
F:1799-2007/Domain: fibrinogen beta/gamma homology <FBG>  
F:38,166,184,327,788,1018,1079,1093,1119,1184,1210,1275,1301,1354,1364,1394,1627,1878,1911  
Query Match 22.3%; Score 110; DB 1; Length 2019;  
Best Local Similarity 35.8%; Pred. No. 0.0073;  
Matches 34; Conservative 9; Mismatches 44; Indels 8; Gaps 4;  
QY 3 DVPRDLEVVAAFTSRLISWNRSGLSQRYRITYGETGNSFPVQFTVP---PWASIAIT 59  
DB 894 DAPRNLRRVSQTDNSITLERNVKNADISYRIKYPISGDDHA-EIDVPKQQATTKTTL 952  
QY 60 SGLKGVVDYITVYAVTQKSDTYKYDDPLISINVRT 94  
DB 953 TGLRPGTEYIGVSAV--KGD--KESDPATINAAAT 983  
RESULT 15  
A31930  
cytotactin - chicken (fragments)  
C:Species: Gallus gallus (chicken)  
C:Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
C:Accession: A31930

R:Jones, F.S.; Burgoon, M.P.; Hoffman, S.; Crossin, K.L.; Cunningham, B.A.; Edelman, G.M.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2186-2190, 1988  
 A:Title: A cDNA clone for cytotoxicin contains sequences similar to epidermal growth factor  
 A:Reference number: A31930; MUID:88176910; PMID:2451243  
 A:Accession: A31930  
 A:Molecule type: mRNA  
 A:Residues: 1-933 <JON>  
 A:Cross-references: UNIPROT:P10039  
 A:Note: the authors' translation of the codons for residues 601-620 differs considerably  
 C:Superfamily: tenascin; EGF homology; fibrinogen beta/gamma homology; fibronectin type  
 C:Keywords: alternative splicing; glycoprotein  
 F:13-39/Domain: EGF homology <EGF>  
 F:134-245/Domain: fibronectin type III repeat homology <FN3A>  
 F:223-307/Domain: fibronectin type III repeat homology <FN3B>  
 F:315-399/Domain: fibronectin type III repeat homology <FN3C>  
 F:407-491/Domain: fibronectin type III repeat homology <FN3D>  
 F:499-576/Domain: fibronectin type III repeat homology <FN3E>  
 F:587-668/Domain: fibronectin type III repeat homology <FN3F>  
 F:765-845/Domain: fibronectin type III repeat homology <FN3G>  
 F:860-933/Domain: fibrinogen beta/gamma homology (fragment) <FBG>  
 F:145,185,293,301,676,688/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.9%; Score 108; DB 2; Length 933;  
 Best Local Similarity 33.7%; Pred. No. 0.0048;  
 Matches 32; Conservative 13; Mismatches 42; Indels 8; Gaps 3;

Qy	3	DVPRDLVVAATPTSRSLISWNRSLQSRYYRITYGETGNSPQVQFTVPW---ASIATI 59
Db	409	DAPNLRKVSQTDNSITLWKFESHANIDNYRIKAPISGGDHT-ELTVPKGNQATTRATL 467
Qy	60	SGLKPGVDYTTIVYAVTDKSDTYKYDDPISINRT 94
Db	468	TGLRPGTEYGIGTAVRQDRES---APATINAGT 498

Search completed: May 18, 2005, 15:47:44  
 Job time : 41 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 18, 2005, 14:59:56 ; Search time 178 Seconds  
(without alignments)  
270.424 Million cell updates/sec

Title: US-09-688-566-81

Perfect score: 494

Sequence: 1 VSDVPRDLEVAATPTSLRLI.....VTDKSTYKYDDPFISINVRT 94

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	361	73.1	1034	2 Q6N084	Q6N084 homo sapien
2	361	73.1	1255	2 Q6MZS0	Q6MZS0 homo sapien
3	361	73.1	2146	2 Q68CX6	Q68CX6 homo sapien
4	361	73.1	2240	2 Q68DP8	Q68DP8 homo sapien
5	361	73.1	2267	2 Q68DP9	Q68DP9 homo sapien
6	361	73.1	2296	2 Q6N0A6	Q6N0A6 homo sapien
7	361	73.1	2357	2 Q68DT4	Q68DT4 homo sapien
8	361	73.1	2386	1 FINC HUMAN	P02751 homo sapien
9	361	73.1	2444	2 Q6N025	Q6N025 homo sapien
10	361	73.1	2477	2 Q6MZU5	Q6MZU5 homo sapien
11	356	72.1	2193	2 Q6MZM7	Q6MZM7 homo sapien
12	354	71.7	2265	1 FINC BOVIN	P07589 bos taurus
13	333	67.4	2477	1 FINC MOUSE	P11276 mus musculus
14	333	67.4	2477	1 FINC RAT	P04937 rattus norv
15	311	63.0	1256	1 FINC CHICK	P11722 gallus gall
16	269	54.5	293	2 Q6XSG0	Q6XSG0 oryctolagus
17	264	53.4	1328	1 FINC PLEWA	Q91289 pleurodeles
18	262	53.0	2481	1 FINC XENILA	Q91740 xenopus lae
19	262	53.0	2481	2 Q6GQA5	Q6GQA5 xenopus lae
20	251	50.8	2478	2 Q91406	Q91406 brachydanio
21	246	49.8	2408	2 Q6JAN2	Q6JAN2 brachydanio
22	153	31.0	68	2 Q28692	Q28692 oryctolagus
23	130	26.3	522	1 FINC HORSE	Q28377 equus caball
24	125	25.3	4006	2 Q35452	Q35452 mus musculus
25	125	25.3	4114	2 Q54796	Q54796 mus musculus
26	124	25.1	4135	2 Q18977	Q18977 bos taurus
27	123	24.9	320	2 Q95KV4	Q95KV4 bos taurus
28	123	24.9	347	2 Q95KV5	Q95KV5 bos taurus
29	123	24.9	426	2 Q9NPK8	Q9NPK8 homo sapien
30	123	24.9	522	1 FINC CANFA	Q28275 canis famil
31	123	24.9	1350	2 Q7T3T6	Q7T3T6 brachydanio

32	123	24.9	4288	2 Q9NPK9	Q9NPK9 homo sapien
33	123	24.9	4289	1 TENX HUMAN	P22105 homo sapien
34	122	24.7	354	2 Q9UQ56	Q9UQ56 homo sapien
35	122	24.7	379	2 Q95617	Q95617 homo sapien
36	121	24.5	1353	2 Q00546	Q00546 gallus gall
37	121	24.5	1746	1 TENX_PIG	Q29116 sus scrofa
38	120.5	24.4	1103	2 Q6MZP4	Q6MZP4 homo sapien
39	119	24.1	810	2 Q8R3F3	Q8R3F3 mus musculus
40	116	23.5	426	2 Q95680	Q95680 homo sapien
41	116	23.5	1356	2 Q00546	Q00546 rattus norv
42	116	23.5	1358	2 Q8BYI9	Q8BYI9 mus musculus
43	115	23.3	1358	2 Q15568	Q15568 homo sapien
44	115	23.3	1358	2 Q92752	Q92752 homo sapien
45	114	23.1	3119	1 CALC_MOUSE	Q60847 mus musculus

ALIGNMENTS

RESULT 1  
Q6N084  
ID Q6N084 PRELIMINARY; PRT; 1034 AA.  
AC Q6N084;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686I11144 (Fragment).  
GN Name=DKFZp686I11144;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Human colon endothel primary cell culture;  
RG The German Human cDNA Consortium;  
RA Wambutt R., Heubner D., Mewes H.W., Well B., Amid C., Oeanger A.,  
RA Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640638; CA545786.1;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR InterPro; IPR002086; Aldehyde dehydrog.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR00083; Fibrinctnl.  
DR InterPro; IPR003962; FNIII subd.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN\_III-like.  
DR Pfam; PF00039; fnl; 3.  
DR Pfam; PF00041; fn3; 9.  
DR PRINTS; PR00012; FNTYPEI.  
DR PRINTS; PR00014; FNTYPEIII.  
DR SMART; SM00058; FN1; 3.  
DR SMART; SM00060; FN3; 8.  
DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF\_1; UNKNOWN\_1.  
DR PROSITE; PS01253; FIBRONECTIN\_1; 3.  
DR PROSITE; PS00853; FN3; 8.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 1034 AA; 113371 MW; 3765128365FD0659 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 1034;  
Best Local Similarity 77.7%; Pred. No. 7.9e-30;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy	1	VSDVPRDLEVAATPTSLRLISWNRSGLQSYRYRTYTGTCGNSPVQFTVPWMSIATIS 60	
Db	216	VSDVPRDLEVAATPTSLRLISWDAPAVTVRYRTYTGTCGNSPVQFTVPGSKSTATIS 275	
Qy	61	GLKPGVDYTTTVAATDKSDTYKYDDPFISINVRT 94	
Db	276	GLKPGVDYTTTVAATGTGDSPASSKPFISINVRT 309	



Qy 61 GLKPGVDYTTIVAVTDSKYDDPISINRYT 94  
||||| :  
Db 1598 GLKPGVDYTTIVAVTGRGDSPASSKPISINRYT 1631

RESULT 6  
Q6NOA6 PRELIMINARY; PRT; 2296 AA.

AC Q6NOA6;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686M04163.  
GN Name=DKFZp686M04163;  
OS Homo sapiens (Human);  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RT TISSUE=Human uterus endothel primary cell culture;  
RG The Human Human cDNA Consortium;  
RA Bloembergen H., Boecker M., Mewes H.W., Weil B., Oanger A.,  
RA Fobo G., Han M., Wiemann S.; GenBank/DBJ databases.  
RL Submitted (AUG-2003) to the ENBL/GenBank/DBJ databases.  
DR EMBL; BX640608; CAE45714.1; -;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR InterPro; IPR002086; Aldehyd dehydrog.  
DR InterPro; IPR006209; EGF-like.  
DR InterPro; IPR000883; Fibrctnl.  
DR InterPro; IPR003961; FN III.  
DR InterPro; IPR008957; FN III-like.  
DR InterPro; IPR000562; FN\_Type\_II.  
DR Pfam; PF00039; fnl; 12.  
DR Pfam; PF00040; fn2; 2.  
DR Pfam; PF00041; fn3; 15.  
DR PRINTS; PR00012; FNTYPEI.  
DR PRINTS; PR00013; FNTYPEII.  
DR ProDom; PD000995; FN\_Type\_II; 2.  
DR SMART; SM00058; FN1\_12.  
DR SMART; SM00059; FN2; 2.  
DR SMART; SM00060; FN3; 15.  
DR PROSITE; PS00687; ALDEHYDE\_DEHYD\_GLU; UNKNOWN\_1.  
DR PROSITE; PS00022; EGF 1; UNKNOWN 2.  
DR PROSITE; PS01253; FIBRONECTIN\_1; 12.  
DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
DR PROSITE; PS00853; FN3; 15.  
KW Hypothetical protein.  
SQ SEQUENCE 2296 AA; 252761 MW; 9AB2D723CC0CED70 CRC64;

Query Match 73.1%; Score 361; DB 2; Length 2296;  
Best Local Similarity 77.7%; Pred No. 2e-29;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

Qy 1 VSDVPRDLVVAATPSRLISWNSGLQSRYRITYGETGNSPVQFTVPNPASIASIATIS 60  
||||| :  
Db 1447 VSDVPRDLVVAATPSLLISWDAPAVTVYRITYGETGNSPVQFTVPNGSKSTATIS 1506

Qy 61 GLKPGVDYTTIVAVTDSKYDDPISINRYT 94  
||||| :  
Db 1507 GLKPGVDYTTIVAVTGRGDSPASSKPISINRYT 1540

RESULT 7  
Q6BDT4 PRELIMINARY; PRT; 2357 AA.

AC Q6BDT4;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein DKFZp686F10164.  
GN Name=DKFZp686F10164;  
OS Homo sapiens (Human);

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Uterus endothel;  
 RG The German cDNA Consortium;  
 RA Koehler K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,  
 RA Fobo G., Han M., Wiemann S.;  
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; CR749281; CAH18136.1; -  
 DR InterPro; IPR002086; Aldhyd dehydrog.  
 DR InterPro; IPR006209; EGF like.  
 DR InterPro; IPR000083; Fibrctn1.  
 DR InterPro; IPR003962; FnIII subd.  
 DR InterPro; IPR003961; FN\_III.  
 DR InterPro; IPR008957; FN\_III-like.  
 DR InterPro; IPR000562; FN\_Type\_II.  
 DR Pfam; PF000039; fn1; 12.  
 DR Pfam; PF00040; fn2; 2.  
 DR Pfam; PF00041; fn3; 15.  
 DR PRINTS; PR00012; FNTYPEI.  
 DR PRINTS; PR00013; FNTYPEII.  
 DR PRINTS; PR00014; FNTYPEIII.  
 DR ProDom; PD000995; FN\_Type\_II; 2.  
 DR SMART; SM00058; FN1; 12.  
 DR SMART; SM00059; FN2; 2.  
 DR SMART; SM00060; FN3; 15.  
 DR PROSITE; PS00687; ALDEHYDE DEHYDR\_GLU; UNKNOWN\_1.  
 DR PROSITE; PS0022; EGF\_1; UNKNOWN\_2.  
 DR PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 DR PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 KW Hypothetical protein.  
 SQ SEQUENCE 2357 AA; 259090 MW; BEAE3990E27B532A CRC64;  
 Query Match 73.1%; Score 361; DB 2; Length 2357;  
 Best Local Similarity 77.7%; Pred. No. 2.1e-29;  
 Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
 QY 1 VSDVPRDLEVAATPTSLISNNRSLQSYRYRITYGTGGNSPVQEFVTPWASITATIS 60  
 Db 1539 VSDVPRDLEVAATPTSLISMDAPAVTVRYRITYGTGGNSPVQEFVTPGSKSTATIS 1598  
 QY 61 GLKPGVDYITVYAVTQDKTYKYDDPISINVRT 94  
 Db 1599 GLKPGVDYITVYAVTGRGDSPASSKPISINVRT 1632  
 RESULT 8  
 FINE\_HUMAN STANDARD; PRT; 2386 AA.  
 AC P02751; O95609; O95610; Q14312; Q14325; Q14336; Q86T27; Q8IV18;  
 AC Q96KP7; Q96KP8; Q96KP9; Q9H1B8; Q9HAP3; Q9UMK2;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fibronectin precursor (FN) (Cold-insoluble globulin) (CIG).  
 GN Name=FN1; Synonyms=FN;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN SEQUENCE FROM N.A. (ISOFORM 2).  
 RX MEDLINE=21600194; PubMed=11737888; DOI=10.1186/bcr325;  
 RA Schor S.L., Schor A.M.;  
 RT "Phenotypic and Genetic alterations in mammary stroma: implications  
 RT for tumour progression";  
 RL Breast Cancer Res. 3:373-379(2001).  
 RN [2]  
 RN SEQUENCE FROM N.A. (ISOFORMS 3; 7 AND 10).  
 RC TISSUE=Cervix;  
 RA Ansoorge W., Krieger S., Regiert T., Rittmueller C., Schwager B.,

RA Mewes H.-W., Weil B., Amid C., Osanger A., Fobo G., Han M.,  
 RA Wiemann S.;  
 RN Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE OF 1-38 FROM N.A.  
 RX MEDLINE=87030890; PubMed=3770189; DOI=10.1016/0014-5793(86)80029-1;  
 RA Gutman A., Yamada K.M., Kornblitt A.R.;  
 RT "Human fibronectin is synthesized as a pre-propolypeptide";  
 RL FEBS Lett. 207:145-148(1986).  
 RN [4]  
 RN SEQUENCE OF 1-49 FROM N.A.  
 RX MEDLINE=87175578; PubMed=3031656;  
 RA Dean D.C., Bowlus C.L., Bourgeois S.;  
 RT "Cloning and analysis of the promotor region of the human fibronectin  
 RT gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:1876-1880(1987).  
 RN [5]  
 RN SEQUENCE OF 28-2386 FROM N.A. (ISOFORM 3).  
 RX MEDLINE=85284965; PubMed=2992939;  
 RA Kornblitt A.R., Umezawa K., Vibe-Pedersen K., Baralle F.E.;  
 RT "Primary structure of human fibronectin: differential splicing may  
 RT generate at least 10 polypeptides from a single gene.";  
 RL EMBO J. 4:1755-1759(1985).  
 RN [6]  
 RN SEQUENCE OF 103-481 AND 2228-2386 FROM N.A. (ISOFORMS 1; 3; 8 AND 9).  
 RC TISSUE=Periphereal blood T-cell, and Umbilical vein endothelial cells;  
 RA Godfrey H.P., Ebrahim A.A.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN SEQUENCE OF 973-2386 FROM N.A. (ISOFORM 3).  
 RX MEDLINE=84272258; PubMed=6462919;  
 RA Kornblitt A.R., Vibe-Pedersen K., Baralle F.E.;  
 RT "Human fibronectin: cell specific alternative mRNA splicing generates  
 RT polypeptide chains differing in the number of internal repeats.";  
 RL Nucleic Acids Res. 12:5853-5868(1984).  
 RN [8]  
 RN SEQUENCE OF 1232-1782 FROM N.A. (ISOFORM 7).  
 RX MEDLINE=88233940; PubMed=3375063;  
 RA Paolella G., Henschliffe C., Sebastio G., Baralle F.E.;  
 RT "Sequence analysis and in vivo expression show that alternative  
 RT splicing of ED-B and ED-A regions of the human fibronectin gene are  
 RT independent events";  
 RL Nucleic Acids Res. 16:3545-3557(1988).  
 RN [9]  
 RN SEQUENCE OF 1257-1365 FROM N.A. (ISOFORM 11).  
 RX MEDLINE=88041070; PubMed=3478690;  
 RA Gutman A., Kornblitt A.R.;  
 RT "Identification of a third region of cell-specific alternative  
 RT splicing in human fibronectin mRNA";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:7179-7182(1987).  
 RN [10]  
 RN SEQUENCE OF 1441-1548.  
 RX MEDLINE=82265604; PubMed=7050098;  
 RA Pierschbacher M.D., Ruoslahti E., Sundelin J., Lind P., Peterson P.A.;  
 RT "The cell attachment domain of fibronectin. Determination of the  
 RT primary structure";  
 RL J. Biol. Chem. 257:9593-9597(1982).  
 RN [11]  
 RN SEQUENCE OF 1448-1540 FROM N.A.  
 RX MEDLINE=83290929; PubMed=6688418;  
 RA Oldberg A., Linney E., Ruoslahti E.;  
 RT "Molecular cloning and nucleotide sequence of a cDNA clone coding for  
 RT the cell attachment domain in human fibronectin";  
 RL J. Biol. Chem. 258:10193-10196(1983).  
 RN [12]  
 RN SEQUENCE OF 1448-1540 FROM N.A.  
 RX MEDLINE=86111901; PubMed=3003095;  
 RA Oldberg A., Ruoslahti E.;  
 RT "Evolution of the fibronectin gene. Exon structure of cell attachment  
 RT domain";  
 RL J. Biol. Chem. 261:2113-2116(1986).  
 RN [13]  
 RN SEQUENCE OF 1594-2386 FROM N.A. (ISOFORM 1).



EX MEDLINE=85280409; PubMed=2992573;  
RA "Bernard M.P., Kolbe M., Weil D., Chu M.-L.;  
RT Human cellular fibronectin: comparison of the carboxyl-terminal  
RT portion with rat identifies primary structural domains separated by  
RT hypervariable regions.";  
RL Biochemistry 24:2698-2704 (1985).  
RN [14]  
RP SEQUENCE OF 1712-1739 FROM N.A.  
RX MEDLINE=87026578; PubMed=3021206;  
RA Sekiguchi K., Klos A.M., Kurachi K., Yoshitake S., Hakomori S.;  
RT "Human liver fibronectin complementary DNAs: identification of two  
RT different messenger RNAs possibly encoding the alpha and beta subunits  
RT of plasma fibronectin.";  
RL Biochemistry 25:4936-4941 (1986).  
RN [15]  
RP SEQUENCE OF 1788-2386 FROM N.A. (ISOFORMS 4; 5 AND 6).  
RC TISSUE=Cartilage;  
RX MEDLINE=22126816; PubMed=12127832; DOI=10.1053/joca.2002.0792;  
RA Parker A.E., Boutell J., Carr A., Maciewicz R.A.;  
RT "Novel cartilage-specific splice variants of fibronectin.";  
RL Osteoarthritis Cartilage 10:528-534 (2002).  
RN [16]  
RP SEQUENCE OF 32-290.  
RX MEDLINE=84032463; PubMed=6630202;  
RA Garcia-Pardo A., Pearlstein E., Frangione B.;  
RT "Primary structure of human plasma fibronectin. The 29,000-dalton NH2-  
RT terminal domain.";  
RL J. Biol. Chem. 258:12670-12674 (1983).  
RN [17]  
RP SEQUENCE OF 109-608, AND COLLAGEN-BINDING.  
RX MEDLINE=87080265; PubMed=3024962;  
RA Owens R.J., Baralle F.E.;  
RT "Mapping the collagen-binding site of human fibronectin by expression  
RT in *Escherichia coli*.";  
RL EMBO J. 5:2825-2830 (1986).  
RN [18]  
RP SULFATION.  
RX MEDLINE=86042625; PubMed=2414772;  
RA Liu M.C., Yu S., Sy J., Redman C.M., Lipmann F.;  
RT "Tyrosine sulfation of proteins from the human hepatoma cell line  
RT HepG2.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:7160-7164 (1985).  
RN [19]  
RP O-GLYCOSYLATION OF THR-2064.  
RX MEDLINE=91190085; PubMed=2012601;  
RA Tresselt T., McCarthy J.B., Calaycay J., Lee T.D., Legesse K.,  
RA Shively J.E., Pande H.;  
RT "Human plasma fibronectin. Demonstration of structural differences  
RT between the A- and B-chains in the III CS region.";  
RL Biochem. J. 274:731-738 (1991).  
RN [20]  
RP FBN1-BINDING SITE.  
RX MEDLINE=93015879; PubMed=1400330;  
RA Balbona K., Tran H., Godyna S., Ingham K.C., Strickland D.K.,  
RA Argaves W.S.;  
RT "Fibulin binds to itself and to the carboxyl-terminal heparin-binding  
RT region of fibronectin.";  
RL J. Biol. Chem. 267:20120-20125 (1992).  
RN [21]  
RP CHARACTERIZATION OF FIBRIN-BINDING SITE 1.  
RX MEDLINE=95081153; PubMed=7989369;  
RA Rostagno A., Williams M.J., Baron M., Campbell I.D., Gold L.I.;  
RT "Further characterization of the NH2-terminal fibrin-binding site on  
RT fibronectin.";  
RL J. Biol. Chem. 269:31938-31945 (1994).  
RN [22]  
RP INTERACTION WITH LGALS3BP.  
RX PubMed=9501082; DOI=10.1093/emboj/17.6.1606;  
RA Sasaki T., Brakebusch C., Engel J., Timpl R.;  
RT "Mac-2 binding protein is a cell-adhesive protein of the extracellular  
RT matrix which self-assembles into ring-like structures and binds beta1  
RT integrins, collagens and fibronectin.";  
RL EMBO J. 17:1606-1613 (1998).

RN [23]  
RP STRUCTURE BY NMR OF 1447-1540.  
RX MEDLINE=92162710; PubMed=1311202;  
RA Baron M., Main A.L., Driscoll P.C., Mardon H.J., Boyd J.,  
RA Campbell I.D.;  
RT "1H NMR assignment and secondary structure of the cell adhesion type  
RT III module of fibronectin.";  
RL Biochemistry 31:2068-2073 (1992).  
RN [24]  
RP STRUCTURE BY NMR OF 1447-1540.  
RX MEDLINE=93046665; PubMed=1423622; DOI=10.1016/0092-8674(92)90600-H;  
RA Main A.L., Harvey T.S., Baron M., Boyd J., Campbell I.D.;  
RT "The three-dimensional structure of the tenth type III module of  
RT fibronectin: an insight into RGD-mediated interactions.";  
RL Cell 71:671-678 (1992).  
RN [25]  
RP STRUCTURE BY NMR OF 182-275.  
RX MEDLINE=94141923; PubMed=8308892;  
RA Williams M.J., Phan I., Harvey T.S., Rostagno A., Gold L.I.,  
RA Campbell I.D.;  
RT "Solution structure of a pair of fibronectin type I modules with  
RT fibrin binding activity.";  
RL J. Mol. Biol. 235:1302-1311 (1994).  
RN [26]  
RP STRUCTURE BY NMR OF 32-92.  
RX MEDLINE=96069779; PubMed=7583666;  
RA Potts J.R., Phan I., Williams M.J., Campbell I.D.;  
RT "High-resolution structural studies of the factor XIIIa crosslinking  
RT site and the first type I module of fibronectin.";  
RL Nat. Struct. Biol. 2:946-950 (1995).  
RN [27]  
Query Match 73.1%; Score 361; DB 1; Length 2386;  
Best Local Similarity 77.7%; Pred. No. 2.1e-29;  
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;  
Qy 1 VSDVPRDLEVAATPTSRLLISWNRSGLQSYRYITYTGTGNSPVQSFVTPPWASIAIS 60  
Db 1447 VSDVPRDLEVAATPTSRLLISWNRSGLQSYRYITYTGTGNSPVQSFVTPPWASIAIS 1506  
Qy 61 GLKPGVDYTTTVAVTQKSDPTKYDDPISINRYT 94  
Db 1507 GLKPGVDYTTTVAVTQKSDPTKYDDPISINRYT 1540  
RESULT 9  
Q6N025 PRELIMINARY; PRT; 2444 AA.  
AC Q6N025;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Hypothetical protein DKFZp686M2451 (Fragment).  
GN Name=DKFZp686M2451;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
SEQUENCE FROM N.A.  
RC TISSUE=Human endometrium carcinoma cell line;  
RG The German Human cDNA Consortium;  
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,  
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BX640731; CA645847.1;  
DR GO; GO:0005576; C:extracellular; IEA.  
DR InterPro; IPR02086; Aldehyd dehydrog.  
DR InterPro; IPR006209; EGF like.  
DR InterPro; IPR000083; Fibronectin.  
DR InterPro; IPR003961; FN\_III-like.  
DR InterPro; IPR008957; FN\_III-like.  
DR InterPro; IPR000562; FN\_Type\_II.

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DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 16.
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DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 12.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 16.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 16.
DR KW Hypothetical protein.
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Best Local Similarity 77.7%; Pred. No. 2.2e-29;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

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Db 1536 VSDVPRDLEVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPWPWASITATIS 1595

QY 61 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 94
Db 1596 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 1629

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Q6MZU5 PRELIMINARY; PRT; 2477 AA.
ID Q6MZU5
AC Q6MZU5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O1166.
GN Name=DKFZp686O1166;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Human endometrium carcinoma cell line;
RG The German Human CDNA Consortium;
RA Bloecker H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640875; CAE4932.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00013; FNTYPEI.
DR PRINTS; PR00014; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 17.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 2477 AA; 272335 MW; D35B8D85C6B18207C CRC64;

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Query Match 73.1%; Score 361; DB 2; Length 2477;
Best Local Similarity 77.7%; Pred. No. 2.2e-29;
Matches 73; Conservative 4; Mismatches 17; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPWPWASITATIS 60
Db 1538 VSDVPRDLEVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPWPWASITATIS 1597

QY 61 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 94
Db 1598 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 1631

RESULT 11
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AC Q6MZM7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686O12165 (Fragment).
GN Name=DKFZp686O12165;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Human uterus endothel primary cell culture;
RG The German Human CDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640999; CAE46002.1; -.
DR GO; GO:000576; C:extracellular; IEA.
DR InterPro; IPR002086; Aldehyd dehydrog.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003962; FNIII subd.
DR InterPro; IPR003961; FN III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR Pfam; PF00039; fn1; 7.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 17.
DR PRINTS; PR00012; FNTYPEI.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00014; FNTYPEIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00058; FN1; 7.
DR SMART; SM00059; FN2; 2.
DR SMART; SM00060; FN3; 17.
DR PROSITE; PS00687; ALDEHYDE DEHYDR GLU; UNKNOWN_1.
DR PROSITE; PS00022; EGF 1; UNKNOWN_2.
DR PROSITE; PS01253; FIBRONECTIN_1; 7.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS00853; FN3; 17.
DR KW Hypothetical protein.
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Best Local Similarity 76.6%; Pred. No. 6.6e-29;
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Db 1285 VSDVPRDLEVAATPTSLISNRSGLQSRYYRITYGETGNSPVQSEFTVPWPWASITATIS 1344

QY 61 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 94
Db 1345 GLKPGVDYTIIVAVYVAVTGRGDSPPASSKPISINVRT 1378

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RESULT 12
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ID_FINC_BOVIN STANDARD; PRT; 2265 AA.
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DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibronectin (FN).
GS Name=FN1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=87054047; PubMed=3780752;
RA Skorstengaard K., Jensen M.S., Sahl P., Petersen T.E., Magnusson S.;
RT "Complete primary structure of bovine plasma fibronectin.";
RL Eur. J. Biochem. 161:441-453(1986).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=83117805; PubMed=6218503;
RA Petersen T.E., Thorgersen H.C., Skorstengaard K., Vibe-Pedersen K.,
RA Sahl P., Sottrup-Jensen L., Magnusson S.;
RT "Partial primary structure of bovine plasma fibronectin: three types
of internal homology.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:137-141(1983).
RN [3]
RP SEQUENCE OF 2170-2265 FROM N.A.
RX MEDLINE=83221567; PubMed=6304699;
RA Kornblith A.R., Vibe-Pedersen K., Baralle F.E.;
RT "Isolation and characterization of cDNA clones for human and bovine
fibronectins.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3218-3222(1983).
CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds
including collagen, fibrin, heparin, DNA, and actin. Fibronectins
are involved in cell adhesion, cell motility, opsonization, wound
healing, and maintenance of cell shape.
CC -!- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
variants, connected by 2 disulfide bonds near the carboxyl ends;
to a lesser extent homodimers.
CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing: Named isoforms=1;
Comment=A number of isoforms are produced. Each of the "extra
domain" and the connecting strand 3 are present in some forms of
fibronectin and absent in others;
Name=1;
CC -!- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
forms), made by fibroblasts, epithelial and other cell types, is
deposited as fibrils in the extracellular matrix.
CC -!- PTM: Sulfated (By similarity).
CC -!- SIMILARITY: Contains 12 fibronectin type I domains.
CC -!- SIMILARITY: Contains 2 fibronectin type II domains.
CC -!- SIMILARITY: Contains 15 fibronectin type III domains.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; X08000; AAA30521.2; -.
PIR; A26452; FNBO.
HSSP; P08253; 1KS0.
InterPro; IPR006209; EGF_like.

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DR InterPro; IPR000083; Fibrnctnl.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR003962; FNIII_subd.
DR Pfam; PF00039; fn1; 12.
DR Pfam; PF00040; fn2; 2.
DR Pfam; PF00041; fn3; 15.
DR PRINTS; PR00012; ENTPEBI.
DR PRINTS; PR00013; ENTPEBII.
DR PRINTS; PR00014; ENTPEBIII.
DR ProDom; PD000995; FN_Type_II; 2.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01253; FIBRONECTIN_1; 12.
DR PROSITE; PS00023; FIBRONECTIN_2; 2.
DR PROSITE; PS08053; FN3; 15.
KW Acute phase; Alternative splicing; Cell adhesion; Cell shape;
KW Direct protein sequencing; Glycoprotein; Heparin-binding;
KW Phosphorylation; Plasma; Pyrrolidone carboxylic acid; Repeat;
KW Sulfation.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DOMAIN 21 241 Fibrin- and heparin-binding 1.
FT DOMAIN 277 577 Collagen-binding.
FT DNA_BIND 876 1141 Cell-attachment.
FT DOMAIN 1236 1509 Heparin-binding 2.
FT DOMAIN 1600 1870 Fibrin-binding 2.
FT DOMAIN 1991 2216 Fibronectin type-I 1.
FT DOMAIN 19 59 Fibronectin type-I 2.
FT DOMAIN 64 107 Fibronectin type-I 3.
FT DOMAIN 108 151 Fibronectin type-I 4.
FT DOMAIN 153 197 Fibronectin type-I 5.
FT DOMAIN 198 242 Fibronectin type-I 6.
FT DOMAIN 275 314 Fibronectin type-II 1.
FT DOMAIN 314 373 Fibronectin type-II 2.
FT DOMAIN 374 438 Fibronectin type-II 3.
FT DOMAIN 437 480 Fibronectin type-I 7.
FT DOMAIN 485 527 Fibronectin type-I 8.
FT DOMAIN 528 571 Fibronectin type-I 9.
FT DOMAIN 576 668 Fibronectin type-III 1.
FT DOMAIN 689 778 Fibronectin type-III 2.
FT DOMAIN 780 867 Fibronectin type-III 3.
FT DOMAIN 877 964 Fibronectin type-III 4.
FT DOMAIN 965 1053 Fibronectin type-III 5.
FT DOMAIN 1056 1141 Fibronectin type-III 6.
FT DOMAIN 1142 1234 Fibronectin type-III 7.
FT DOMAIN 1235 1325 Fibronectin type-III 8.
FT DOMAIN 1326 1415 Fibronectin type-III 9.
FT DOMAIN 1416 1505 Fibronectin type-III 10.
FT DOMAIN 1510 1599 Fibronectin type-III 11.
FT DOMAIN 1602 1689 Fibronectin type-III 12.
FT DOMAIN 1692 1780 Fibronectin type-III 13.
FT DOMAIN 1781 1870 Fibronectin type-III 14.
FT DOMAIN 1871 1990 Connecting strand 3 (CS-3) (V region).
FT DOMAIN 1979 2069 Fibronectin type-III 15.
FT DOMAIN 2083 2127 Fibronectin type-I 10.
FT DOMAIN 2128 2170 Fibronectin type-I 11.
FT DOMAIN 2172 2215 Fibronectin type-I 12.
FT SITE 1493 1495 Cell attachment site.
FT DISULFID 21 47
FT DISULFID 45 56
FT DISULFID 66 94
FT DISULFID 92 104
FT DISULFID 110 138
FT DISULFID 136 148
FT DISULFID 155 184
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FT DISULFID 403 430  
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 FT DISULFID 487 514  
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 FT DISULFID 530 558  
 FT DISULFID 556 568  
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 FT DISULFID 2112 2124  
 FT DISULFID 2130 2157  
 FT DISULFID 2155 2167  
 FT DISULFID 2174 2200  
 FT DISULFID 2198 2209  
 FT DISULFID 2246 2246  
 FT DISULFID 2250 2250  
 FT MOD\_RES 845 845  
 FT MOD\_RES 850 850  
 FT CARBOHYD 399 399  
 FT CARBOHYD 497 497  
 FT CARBOHYD 511 511  
 FT CARBOHYD 846 846  
 FT CARBOHYD 976 976  
 FT CARBOHYD 1213 1213  
 FT CARBOHYD 1987 1987  
 FT CARBOHYD 1943 1943  
 FT CARBOHYD 1944 1944  
 FT MOD\_RES 2263 2263  
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 Best Local Similarity 74.5%; Pred. No. 1.1e-28;  
 Matches 70; Conservative 7; Mismatches 17; Indels 0; Gaps 0;  
  
 QY 1 VSDVPRDLVVAATPSRLISWNRSLGQRYRYRITYGTGNSPVQEFVTPVWSTATIS 60  
 Db 1416 VSDVPRDLVVAATPSRLISWNRSLGQRYRYRITYGTGNSPVQEFVTPVWSTATIS 1475  
  
 QY 61 GLKPGVDYITVAVYVTKDQTYKYDDPISINVRT 94  
 Db 1476 GLKPGVDYITVAVYVTKDQTYKYDDPISINVRT 1509  
  
 RESULT 13  
 FINC MOUSE  
 ID FINC MOUSE STANDARD; PRT; 2477 AA.  
 AC F11276; Q61569; Q61569; Q64233; Q80014;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Fibronectin precursor (FN).  
 GN Names=fn1;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 [1]  
 RN SEQUENCE OF 1-920 FROM N.A.  
 RC STRAIN=FVB/N-3; TISSUE=Breast tumor;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Rosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villaola D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Snailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE OF 1-28 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=94131313; PubMed=8299972; DOI=10.1016/0378-1119(93)90036-3;  
 RA Talts J.F., Weller A., Timpl R., Ekblom M., Ekblom P.;  
 RT "Regulation of mesenchymal extracellular matrix protein synthesis by  
 transforming growth factor-beta and glucocorticoids in tumor stroma."; J.  
 Cell Sci. 108:2153-2162(1995).  
 RN [4]  
 RP SEQUENCE OF 899-2376 FROM N.A.  
 RA Gorski G., Aros M., Norton P.;  
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 2375-2477 FROM N.A.  
 RX MEDLINE=88124987; PubMed=3124113;  
 RA Blatti S.P., Foster D.N., Ranganathan G., Moses H.L., Getz M.J.;  
 RT "Induction of fibronectin gene transcription and mRNA is a primary  
 response to growth-factor stimulation of AKR-2B cells."; Proc. Natl. Acad. Sci. U.S.A. 85:1119-1123(1988).  
 RN [6]  
 RP SEQUENCE OF 2375-2477 FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=93011702; PubMed=1327855;  
 RA Khandjian E.W., Salomon C., Leonard N., Tremblay S., Turler H.;  
 RT "Fibronectin gene expression in proliferating, quiescent, and SV40-  
 infected mouse kidney cells."; Exp. Cell Res. 202:464-470(1992).  
 RN [7]  
 RP STRUCTURE BY NMR OF 1447-1630.  
 RX MEDLINE=98205278; PubMed=9533887; DOI=10.1006/jmbi.1998.1616;  
 RA Copie V., Tomita Y., Akiyama S.K., Aota S., Yamada K.M., Venable R.M.,  
 RA Pastor R.W., Krueger S., Torchia D.A.;  
 RT "Solution structure and dynamics of linked cell attachment modules of  
 mouse fibronectin containing the RGD and synergy regions: comparison  
 with the human fibronectin crystal structure."; J. Mol. Biol. 277:663-682(1998).  
 RN [8]  
 RP DOWN-REGULATION BY GLUCOCORTICOID.  
 RX MEDLINE=21600963; PubMed=11737251;  
 RA Gu Y.-C., Talts J.F., Gullberg D., Timpl R., Ekblom M.;  
 RT "Glucocorticoids down-regulate the extracellular matrix proteins  
 fibronectin, fibulin-1 and fibulin-2 in bone marrow stroma."; Eur. J. Haematol. 67:176-184(2001).  
 CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds  
 including collagen, fibrin, heparin, DNA, and actin. Fibronectins  
 are involved in cell adhesion, cell motility, opsonization, wound  
 healing, and maintenance of cell shape.  
 CC -!- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced  
 variants, connected by 2 disulfide bonds near the carboxyl ends;  
 to a lesser extent homodimers. Interacts with FBLN1 and LGALS3BP  
 (by similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=alternative splicing; Named isoforms=1;  
 CC Comment=A number of isoforms are produced. Each of the "extra  
 domain" and the connecting strand 3 are present in some forms of  
 fibronectin and absent in others;  
 CC Name=1;  
 CC ISOID=P11276-1; Sequences=Displayed;  
 CC -!- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted

CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric  
 CC forms), made by fibroblasts, epithelial and other cell types, is  
 CC deposited as fibrils in the extracellular matrix.  
 CC -!- INDUCTION: Glucocorticoids suppressed mRNA expression and protein  
 CC synthesis.  
 CC -!- PTM: Sulfated (By similarity).  
 CC -!- SIMILARITY: Contains 12 fibronectin type I domains.  
 CC -!- SIMILARITY: Contains 2 fibronectin type II domains.  
 CC -!- SIMILARITY: Contains 17 fibronectin type III domains.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; BC051082; AAH51082.1; -;  
 CC EMBL; Z22729; CAA80422.1; -;  
 CC EMBL; X82402; CAA57796.1; -;  
 CC EMBL; X93167; CAA63654.1; -;  
 CC EMBL; M18194; AAA37636.1; -;  
 CC EMBL; S45680; AAB23491.1; -;  
 CC PIR; A49173; A49173.  
 CC PIR; I48349; I48349.  
 CC PDB; 1MFN; NMR; @=1446-1630.  
 CC PDB; 2MFN; NMR; @=1446-1630.  
 CC MGD; MGI:95566; Fnl.  
 CC GO; GO:0007044; P:cell adhesion; IDA.  
 CC GO; GO:0007044; P:cell-substrate junction assembly; IDA.  
 CC GO; GO:0042060; P:wound healing; IMP.  
 CC InterPro; IPR006209; EGF like.  
 CC InterPro; IPR000083; Fibrinctn1.  
 CC InterPro; IPR003962; FNIII subd.  
 CC InterPro; IPR003961; FN III.  
 CC InterPro; IPR008957; FN-III-like.  
 CC InterPro; IPR000562; FN\_Type\_II.  
 CC Pfam; PF00039; fn1; 12.  
 CC Pfam; PF00040; fn2; 2.  
 CC Pfam; PF00041; fn3; 17.  
 CC PRINTS; PR00014; FNTYPEIII.  
 CC ProDom; PD000995; FN\_Type\_II; 2.  
 CC PROSITE; PS00022; EGF\_1; 2.  
 CC PROSITE; PS01253; FIBRONECTIN\_1; 12.  
 CC PROSITE; PS00023; FIBRONECTIN\_2; 2.  
 CC PROSITE; PS00853; FN3; 17.  
 CC 3D-structure; Acute phase; Alternative splicing; Cell adhesion;  
 CC Glycoprotein; Heparin-binding; Phosphorylation; Plasma; Repeat;  
 CC Signal; Sulfation.  
 CC SIGNAL 1 32 By similarity.  
 CC CHAIN 33 2477 Fibronectin.  
 CC DOMAIN 53 273 Fibrin- and heparin-binding 1.  
 CC DOMAIN 308 608 Collagen-binding.  
 CC DNA\_BIND 906 1171  
 CC DOMAIN 1357 1630 Cell-attachment.  
 CC DOMAIN 1811 2081 Heparin-binding 2.  
 CC DOMAIN 2296 2427 Fibrin-binding 2.  
 CC DOMAIN 51 96 Fibronectin type-I 1.  
 CC DOMAIN 96 140 Fibronectin type-I 2.  
 CC DOMAIN 140 185 Fibronectin type-I 3.  
 CC DOMAIN 185 230 Fibronectin type-I 4.  
 CC DOMAIN 230 272 Fibronectin type-I 5.  
 CC DOMAIN 306 343 Fibronectin type-I 6.  
 CC DOMAIN 345 404 Fibronectin type-II 1.  
 CC DOMAIN 405 469 Fibronectin type-II 2.  
 CC DOMAIN 468 516 Fibronectin type-I 7.  
 CC DOMAIN 516 559 Fibronectin type-I 8.  
 CC DOMAIN 559 602 Fibronectin type-I 9.  
 CC DOMAIN 607 699 Fibronectin type-III 1.  
 CC DOMAIN 719 808 Fibronectin type-III 2.  
 CC DOMAIN 810 897 Fibronectin type-III 3.  
 CC DOMAIN 905 994 Fibronectin type-III 4.

FT DOMAIN 995 1083 Fibronectin type-III 5.  
 FT DOMAIN 1091 1171 Fibronectin type-III 6.  
 FT DOMAIN 1172 1264 Fibronectin type-III 7.  
 FT DOMAIN 1265 1355 Fibronectin type-III 8 (extra domain 1).  
 FT DOMAIN 1356 1446 Fibronectin type-III 9.  
 FT DOMAIN 1447 1536 Fibronectin type-III 10.  
 FT DOMAIN 1537 1626 Fibronectin type-III 11.  
 FT DOMAIN 1631 1720 Fibronectin type-III 12.  
 FT DOMAIN 1721 1810 Fibronectin type-III 13 (extra domain 2).  
 FT DOMAIN 1813 1900 Fibronectin type-III 14.  
 FT DOMAIN 1903 1991 Fibronectin type-III 15.  
 FT DOMAIN 1992 2081 Fibronectin type-III 16.  
 FT DOMAIN 2082 2201 Connecting strand 3 (CS-3) (V region).  
 FT DOMAIN 2190 2280 Fibronectin type-III 17.  
 FT DOMAIN 2294 2338 Fibronectin type-I 10.  
 FT DOMAIN 2339 2381 Fibronectin type-I 11.  
 FT DOMAIN 2383 2426 Fibronectin type-I 12.  
 FT SITE 1614 1616 Cell attachment site.  
 FT SITE 2181 2183 Cell attachment site.  
 FT DISULFID 53 79 By similarity.  
 FT DISULFID 77 88 By similarity.  
 FT DISULFID 98 126 By similarity.  
 FT DISULFID 124 136 By similarity.  
 FT DISULFID 142 170 By similarity.  
 FT DISULFID 168 180 By similarity.  
 Query Match 67.4%; Score 333; DB 1; Length 2477;  
 Best Local Similarity 67.0%; Pred. No. 2.3e-26;  
 Matches 63; Conservative 11; Mismatches 20; Indels 0; Gaps 0;  
 Qy 1 VSDVPRDLEVVAAPTSLRLISWNRSGLQSYRYRITYGETGNSPVQETVPPWASIAITIS 60  
 Db 1537 VSDIPRDLVIASTPTSLISWEPPAVSVRYRITYGETGNSPVQETVPPGSKSTATIN 1596  
 Qy 61 GLKPGVDYTTVYAVTDKSTYKYDDPDISINYRT 94  
 Db 1597 NIKPGADYTTLYAVTGRGDSPPASSKPVSYNYKT 1630  
 RESULT 14  
 FINE\_RAT  
 ID\_FINE\_RAT STANDARD; PRT; 2477 AA.  
 AC P04937; O6LXD9;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 25-JAN-2005 (Rel. 46, Last annotation update)  
 DE Fibronectin precursor (FN).  
 GN Name=Fnl;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Liver;  
 RX MEDLINE=88054951; PubMed=2445560;  
 RA Schwarzbauer J.E., Patel R.S., Fonda D., Hynes R.O.;  
 RT "Multiple sites of alternative splicing of the rat fibronectin gene  
 transcript.";  
 RL EMO J. 6:2573-2580(1987).  
 RN [2]  
 RP SEQUENCE OF 1-139 AND 2382-2477 FROM N.A.  
 RC STRAIN=Fischer; TISSUE=Liver;  
 RX MEDLINE=88054950; PubMed=3119123;  
 RA Patel R.S., Odermatt E., Schwarzbauer J.E., Hynes R.O.;  
 RT "Organization of the fibronectin gene provides evidence for exon  
 shuffling during evolution.";  
 RL EMO J. 6:2565-2572(1987).  
 RN [3]  
 RP SEQUENCE OF 1586-2477 FROM N.A.  
 RX MEDLINE=84082067; PubMed=6317187; DOI=10.1016/0092-8674(83)90175-7;  
 RA Schwarzbauer J.E., Tamkun J.W., Lemischka I.R., Hynes R.O.;  
 RT "Three different fibronectin mRNAs arise by alternative splicing

RT within the coding region.";

RL Cell 35:421-431(1983).

RN [4]

RP SEQUENCE OF 1722-1810 FROM N.A., AND ALTERNATIVE SPLICING.

RX PubMed=3663113;

RA Odermatt E., Tamkun J.W., Hynes R.O.;

RT "Repeating modular structure of the fibronectin gene: relationship to

RT protein structure and subunit variation.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:6571-6575(1985).

RN [5]

RP SEQUENCE OF 2052-2237 FROM N.A., AND ALTERNATIVE SPLICING.

RX PubMed=6089177;

RA Tamkun J.W., Schwarzbauer J.E., Hynes R.O.;

RT "A single rat fibronectin gene generates three different mRNAs by

RT alternative splicing of a complex exon.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5140-5144(1984).

RN [6]

RP SEQUENCE OF 1183-1192; 1385-1399 AND 2287-2300, AND INTERACTION WITH

RX AMBP.

RX PubMed=7519849;

RA Falkenberg C., Enghild J.J., Thøgersen I.B., Salvesen G.,

RT Akerstrom B.;

RT "Isolation and characterization of fibronectin-alpha 1-microglobulin

RT complex in rat plasma.";

RL Biochem. J. 301:745-751(1994).

CC -!- FUNCTION: Fibronectins bind cell surfaces and various compounds

CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins

CC are involved in cell adhesion, cell motility, opsonization, wound

CC healing, and maintenance of cell shape.

CC -!- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced

CC variants, connected by 2 disulfide bonds near the carboxyl ends;

CC to a lesser extent homodimers. Interacts with FBLN1, AMBP and

CC LGALS3BP (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted; extracellular matrix.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Comment=Each of the "extra domain" and the connecting strand 3

CC are present in some forms of fibronectin and absent in others;

CC Name=1;

CC IsoId=P04937-1; Sequence=Displayed;

CC Name=2; Synonyms=FNIII-13-less;

CC IsoId=P04937-2; Sequence=VSP\_003258;

CC Name=3; Synonyms=Lambda-RLF4-5;

CC IsoId=P04937-3; Sequence=VSP\_003259;

CC Name=4; Synonyms=Lambda-RLF6;

CC IsoId=P04937-4; Sequence=VSP\_003260;

CC -!- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted

CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric

CC forms), made by fibroblasts, epithelial and other cell types, is

CC deposited as fibrils in the extracellular matrix.

CC -!- PTM: Sulfated (By similarity).

CC -!- SIMILARITY: Contains 12 fibronectin type I domains.

CC -!- SIMILARITY: Contains 2 fibronectin type II domains.

CC -!- SIMILARITY: Contains 17 fibronectin type III domains.

CC -----

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CC -----

DR EMBL; X15906; CAA34020.1; -.

DR EMBL; L29191; AAA41166.1; -.

DR EMBL; L00191; AAA41166.1; JOINED.

DR EMBL; L29191; AAA41167.1; -.

DR EMBL; L00191; AAA41167.1; JOINED.

DR EMBL; L29191; AAA41168.1; -.

DR EMBL; L00191; AAA41168.1; JOINED.

DR EMBL; M11750; AAA41170.1; -.

DR EMBL; X05831; CAA29278.1; -.

DR EMBL; X05832; CAA29279.1; -.

DR EMBL; X05833; CAA29280.1; -.

DR EMBL; X05834; CAA29281.1; -.

DR PIR; S14428; S14428.

DR HSP; P08253; 1KS0.

DR RGD; 2624; FNI.

DR InterPro; IPR006209; EGF like.

DR InterPro; IPR000083; Fibrinctn1.

DR InterPro; IPR003962; FNIII subd.

DR InterPro; IPR003961; FN III.

DR InterPro; IPR008957; FN-III-like.

DR InterPro; IPR000562; FN\_Type-II.

DR Pfam; PF00039; fn1; 12.

DR Pfam; PF00040; fn2; 2.

DR Pfam; PF00041; fn3; 17.

DR PRINTS; PR00013; FNTYPEII.

DR PRINTS; PR00014; FNTYPEIII.

DR ProDom; PD000995; FN\_Type\_II; 2.

DR PROSITE; PS00022; EGF 1; 2.

DR PROSITE; PS01253; FIBRONECTIN\_1; 12.

DR PROSITE; PS00023; FIBRONECTIN\_2; 2.

DR PROSITE; PS50853; FN3; 17.

DR Acute phase; Alternative splicing; Cell adhesion;

DR Direct protein sequencing; Glycoprotein; Heparin-binding;

DR Phosphorylation; Plasma; Repeat; Signal; Sulfation.

FT SIGNAL 1 32

FT CHAIN 33 2477 Fibronectin.

FT DOMAIN 53 273 Fibrin- and heparin-binding 1.

FT DOMAIN 308 608 Collagen-binding.

FT DNA\_BIND 906 1171

FT DOMAIN 1357 1630 Cell-attachment.

FT DOMAIN 1811 2081 Heparin-binding 2.

FT DOMAIN 2296 2427 Fibrin-binding 2.

FT DOMAIN 51 91 Fibronectin type-I 1.

FT DOMAIN 96 139 Fibronectin type-I 2.

FT DOMAIN 140 183 Fibronectin type-I 3.

FT DOMAIN 185 229 Fibronectin type-I 4.

FT DOMAIN 230 274 Fibronectin type-I 5.

FT DOMAIN 306 345 Fibronectin type-I 6.

FT DOMAIN 345 404 Fibronectin type-II 1.

FT DOMAIN 405 469 Fibronectin type-II 2.

FT DOMAIN 511 558 Fibronectin type-I 7.

FT DOMAIN 559 602 Fibronectin type-I 8.

FT DOMAIN 607 699 Fibronectin type-I 9.

FT DOMAIN 719 808 Fibronectin type-III 1.

FT DOMAIN 810 897 Fibronectin type-III 2.

FT DOMAIN 907 994 Fibronectin type-III 3.

FT DOMAIN 1091 1171 Fibronectin type-III 4.

FT DOMAIN 1172 1264 Fibronectin type-III 5.

FT DOMAIN 1265 1355 Fibronectin type-III 6.

FT DOMAIN 1356 1446 Fibronectin type-III 7.

FT DOMAIN 1447 1536 Fibronectin type-III 8.

FT DOMAIN 1537 1626 Fibronectin type-III 9.

FT DOMAIN 1631 1720 Fibronectin type-III 10.

FT DOMAIN 1721 1810 Fibronectin type-III 11.

FT DOMAIN 1813 1900 Fibronectin type-III 12.

FT DOMAIN 1903 1991 Fibronectin type-III 13 (extra domain 2).

FT DOMAIN 1992 2081 Fibronectin type-III 14.

FT DOMAIN 2082 2201 Fibronectin type-III 15.

FT DOMAIN 2190 2280 Fibronectin type-III 16.

FT DOMAIN 2284 2338 Fibronectin type-III 17.

FT DOMAIN 2339 2381 Fibronectin type-I 10.

FT DOMAIN 2383 2426 Fibronectin type-I 12.

FT SITE 1614 1616 Cell attachment site.

FT SITE 2181 2183 Cell attachment site.

FT DISULFID 53 79 By similarity.

FT DISULFID 77 88 By similarity.

FT DISULFID 98 126 By similarity.

FT DISULFID 124 136 By similarity.

FT DISULFID 142 170 By similarity.

FT DISULFID 168 180 By similarity.

FT DISULFID 187 216 By similarity.

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FT DISULFID 214 226 By similarity.
FT DISULFID 232 261 By similarity.
FT DISULFID 259 271 By similarity.
FT DISULFID 308 335 By similarity.
FT DISULFID 333 342 By similarity.
FT DISULFID 360 386 By similarity.
FT DISULFID 374 401 By similarity.
FT DISULFID 420 446 By similarity.
FT DISULFID 434 461 By similarity.
FT DISULFID 470 498 By similarity.
FT DISULFID 496 508 By similarity.
FT DISULFID 518 545 By similarity.
FT DISULFID 543 555 By similarity.
FT DISULFID 561 589 By similarity.
FT DISULFID 587 599 By similarity.
FT DISULFID 2296 2325 By similarity.
FT DISULFID 2323 2335 By similarity.
FT DISULFID 2341 2368 By similarity.
FT DISULFID 2366 2378 By similarity.
FT DISULFID 2385 2409 By similarity.
FT DISULFID 2407 2423 By similarity.
FT DISULFID 2458 Interchain (with C-2462).

Query Match 67.4%; Score 333; DB 1; Length 2477;
Best Local Similarity 68.1%; Pred. NO. 2.3e-26;
Matches 64; Conservative 10; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VSDPRDELVAAPTSLISWNSGLQSRVYRYTGTGGNSPVOEFTVPPWASIAIIS 60
Db 1537 VSDPRDELVAAPTSLISWNSGLQSRVYRYTGTGGNSPVOEFTVPPWASIAIIS 1596

Qy 61 GLKPGVDYITVYAVTKSDTYKYDDPISINRYT 94
Db 1597 NIKPGADYITVYAVTGRGDSPPASSKPVSYNYQT 1630

RESULT 15
ID_FINC CHICK STANDARD; PRT; 1256 AA.
AC P11722; Q90921;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Fibronectin (FN) (Fragments).
GN Name=FN1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE OF 1-50 FROM N.A.
RX MEDLINE=83117850; PubMed=6572007;
RA Hirano H., Yamada Y., Sullivan M., de Crombrughe B., Pastan I.,
RA Yamada K.M.;
RT "Isolation of genomic DNA clones spanning the entire fibronectin
RT gene."
RL Proc. Natl. Acad. Sci. U.S.A. 80:46-50(1983).
RN [2]
RP SEQUENCE OF 51-1256 FROM N.A.
RC STRAIN=white leghorn;
RA Norton P.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 227-415 FROM N.A.
RX MEDLINE=96183658; PubMed=8603103; DOI=10.1016/0167-4889(95)00183-2;
RA Gehris A.L., Brandli D.W., Lewis S.D., Bennett V.D.;
RT "The exon encoding the fibronectin type III-9 repeat is constitutively
RT included in the mRNA from chick limb mesenchyme and cartilage."
RN Biochim. Biophys. Acta 1311:5-12(1996).
RN [4]
RP SEQUENCE OF 327-599 FROM N.A.
RX MEDLINE=88050950; PubMed=2823899; DOI=10.1016/0167-4781(87)90070-4;

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RA Kubomura S., Obara M., Karasaki Y., Taniguchi H., Gotoh S., Tsuda T.,
RA Higashi K., Ohsato K., Hiarno H.;
RT "Genetic analysis of the cell binding domain region of the chicken
RL fibronectin gene."
RN Biochim. Biophys. Acta 910:171-181(1987).
RP [5]
RX SEQUENCE OF 413-1256 FROM N.A.
RA MEDLINE=88142820; PubMed=2830487;
RT Norton P.A., Hynes R.O.;
RL "Alternative splicing of chicken fibronectin in embryos and in normal
RN and transformed cells."
CC Mol. Cell. Biol. 7:4297-4307(1987).
CC -|- FUNCTION: Fibronectins bind cell surfaces and various compounds
CC including collagen, fibrin, heparin, DNA, and actin. Fibronectins
CC are involved in cell adhesion, cell motility, opsonization, wound
CC healing, and maintenance of cell shape.
CC -|- SUBUNIT: Mostly heterodimers or multimers of alternatively spliced
CC variants, connected by 2 disulfide bonds near the carboxyl ends;
CC to a lesser extent homodimers.
CC -|- SUBCELLULAR LOCATION: Secreted; extracellular matrix.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced. Each of the "extra
CC domain" and the connecting strand 3 are present in some forms of
CC fibronectin and absent in others;
CC Name=1;
CC IsoId=P11722-1; Sequence=Displayed;
CC -|- TISSUE SPECIFICITY: Plasma FN (soluble dimeric form) is secreted
CC by hepatocytes. Cellular FN (dimeric or cross-linked multimeric
CC forms), made by fibroblasts, epithelial and other cell types, is
CC deposited as fibrils in the extracellular matrix.
CC -|- PTM: Sulfated (By similarity).
CC -|- SIMILARITY: Contains at least 2 fibronectin type I domains.
CC -|- SIMILARITY: Contains at least 11 fibronectin type III domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; V00432; CAA23714.1; -
DR EMBL; U21327; AAA73566.1; -
DR EMBL; X06533; CAA29781.1; -
DR EMBL; M26186; AAA48772.1; ALT_SEQ.
DR EMBL; U20386; AAB01062.1; -
DR PIR; A28512; A28512.
DR PIR; A29355; A29355.
DR PIR; S71465; S71465.
DR HSSP; P02751; 1FNH.
DR InterPro; IPR000083; Fibnctnl.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR000562; FN Type II.
DR InterPro; IPR003962; FNIII_subd.
DR PRINTS; PR00012; ENTPEI.
DR PRINTS; PR00014; ENTPEIII.
DR PROSITE; PS01253; FIBRONECTIN_1; 2.
DR PROSITE; PS00023; FIBRONECTIN_2; PARTIAL.
DR PROSITE; PS00853; FN3; 11.
DR Acute phase; Alternative splicing; Cell adhesion; Glycoprotein;
KW Heparin-binding; Plasma; Repeat; Sulfation.
FT NON_TER 1
FT NON_CONS 50 51
FT DOMAIN 51 143 Fibronectin type-III 1.
FT DOMAIN 144 234 Fibronectin type-III 2.
FT DOMAIN 235 325 Fibronectin type-III 3.
FT DOMAIN 236 509 Cell-attachment.
FT DOMAIN 690 961 Heparin-binding 2.
FT DOMAIN 1153 1226 Fibrin-binding 2 (By similarity).
FT DOMAIN 326 415 Fibronectin type-III 4.
FT DOMAIN 416 505 Fibronectin type-III 5.

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FT DOMAIN 510 599 Fibronection type-III 6 (extra domain 1).
FT DOMAIN 600 689 Fibronection type-III 7 (extra domain 2).
FT DOMAIN 692 779 Fibronection type-III 8.
FT DOMAIN 782 871 Fibronection type-III.
FT DOMAIN 872 961 Fibronection type-III.
FT DOMAIN 962 1082 Connecting strand 3 (CS-3) (V region).
FT DOMAIN 1071 1160 Fibronection type-III 11.
FT DOMAIN 1174 1218 Fibronection type-I.
FT DOMAIN 1219 >1256 Fibronection type-I.
FT SITE 493 495 Cell attachment site.
FT DISULFID 1176 1205 By similarity.
FT DISULFID 1203 1215 By similarity.
FT DISULFID 1221 1248 By similarity.
FT CARBOHYD 122 122 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 1078 1078 N-linked (GlcNAc...) (By similarity).
FT CARBOHYD 1034 1034 O-linked (GalNAc...) (By similarity).
FT CARBOHYD 1035 1035 O-linked (GalNAc...) (By similarity).
FT CONFLICT 516 516 Q -> P (in Ref. 4).
FT CONFLICT 569 572 EGLQ -> QGLE (in Ref. 4).
FT NON_TER 1256 1256
SQ SEQUENCE 1256 AA; 137435 MW; 345A4CA0E4D71D9B CRC64;

Query Match 63.0%; Score 311; DB 1; Length 1256;
Best Local Similarity 64.9%; Pred. No. 2.4e-24;
Matches 61; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 1 VSDVPRDLEVAATPTSRLLSNRSLQSRYYRITYGETGNSPVOEFTVPPWASTATIS 60
Db 416 VSDVPRDLEVNPTSPTSLSLEISWDAPAVTVYRITYGETGGSPVOEFTVPGTMSRATIT 475

QY 61 GLKPGVDYTIIVYAVTDKSDTYKYDDPISINVRT 94
Db 476 GLKPGVDYTIIVYAVTGRGDSPASSKPVIVTYKT 509
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Search completed: May 18, 2005, 15:34:55  
Job time : 181 secs